

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2002, 15:43:08 Search time 17.84 Seconds

(without alignments) 1842 071 Million cell updates/sec

File: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLISAPGNISLCTRD.....SQDNKKKKQDGDHNEETPM 342

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues 283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200200000

Post-processing: Minimum Match 98

Maximum Match 100%

Listing first 45 summaries

Database: 1: p1r71:*

2: p1r1:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	394	22.2	342	2	A40191 platelet activating factor receptor
2	392.5	22.1	342	2	A40191 platelet activating factor receptor
3	379.5	21.3	342	2	B45680 G protein-coupled platelet activator
4	366	20.6	341	2	S63666 platelet activator
5	362	20.4	341	2	S43352 platelet activator
6	357.5	20.1	308	2	I50241 G protein-coupled
7	349	19.1	359	2	S15403 angiotensin II receptor
8	344	19.0	344	2	T09408 angiotensin II receptor
9	329	18.5	359	2	T09418 angiotensin II receptor
10	326	18.3	359	2	S44425 angiotensin II receptor
11	325.5	18.3	359	2	I48705 angiotensin II receptor
12	325	18.3	359	2	A48857 angiotensin II receptor
13	321	18.1	359	2	T01104 angiotensin II receptor
14	319	17.9	359	2	T05549 angiotensin II receptor
15	319	17.9	359	2	A42656 angiotensin II receptor
16	319	17.9	359	2	A42134 angiotensin II receptor
17	318	17.9	359	2	J01194 angiotensin II receptor
18	318	17.9	359	2	JH0621 angiotensin II receptor
19	317.5	17.9	355	2	S68508 G protein-coupled
20	317.5	17.9	358	2	I56517 mu opiate receptor
21	314.5	17.7	358	2	I56504 mu opiate receptor
22	314	17.7	359	2	J01516 angiotensin II receptor
23	313.5	17.6	388	2	I38435 angiotensin II receptor
24	310.5	17.4	342	2	JN0694 angiotensin II receptor
25	309	17.4	392	2	S65693 mu opiate receptor
26	309	17.4	400	2	I56553 mu opiate receptor
27	306	17.2	397	2	S66518 platelet activating factor receptor
28	304.5	17.1	398	2	A57510 mu opiate receptor
29	299	16.8	380	2	J02434 kappa opiate receptor

ALIGNMENTS

RESULT 1

A40191
platelet activating factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28 Aug 1992 #text_change 20 Jun 2000
C:Accession: A40191; J00479; J01369; A42841; J01923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet activating factor receptor: cDNA cloning, cell
A:Reference number: A40191; M01D:92250505
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <KUN>
A:Cross-References: GR-M76674; NID:9456293; PIDN:AAA60002; PID:9456294
R:Ye, R.D.; Prossnitz, F.R.; Zou, A.; Cochrane, C.G.
Biochem Biophys Res Commun 190, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for platelet activating factor
A:Reference number: JH0479; M01D:92028922
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YER>
A:Cross-References: GR-M80436; NID:9189547; PIDN:AAA60001; PID:9189548
A:Experimental source: granulocyte, cell line HL-60 all
R:Nakamura, M.; Honda, S.; Izumi, T.; Sakonaka, C.; Mutoh, H.; Minami, M.; Bito, H.;
T. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet activating factor receptor from
A:Reference number: A41079; M01D:92041873
A:Accession: A41079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-References: GR-J00404; NID:9219975; PIDN:AAA01096; PID:9219976
R:Soumireu, T.; Tsuchimochi, H.; McGreger, C.G.A.; Mutoh, H.; Shimizu, I.; Kurachi, Y.
Biochem Biophys Res Commun 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet activating factor receptor
A:Reference number: J01359; M01D:93112021
A:Accession: J01359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A:Note: The authors translated the codon AAT for residue 316 as lys
R:Severin, C.E.; Schweickart, V.L.; Gdalska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intron
A:Reference number: A42831; M01D:92347886
A:Accession: A42831
A:Molecule type: DNA
A:Residues: 1-226, TG, 229-342 <SEV>
A:Cross-References: GR-M8177; NID:9196697; PIDN:AAA02141; PID:9196698
R:Chao, P.H.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

Active cloning of a human platelet activating factor receptor gene: evidence for an

Accession number: 151923; MIM:93192035

Accession: 151923

Accession: preliminary; translated from CH/EMH/DBHJ

Accession type: DNA

Accession: 151923; RES

Accession: 151923; GB: S6394; NID: 4298580; PID: A45755.1; PID: 4298581

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Db 292 FTVCAMNFCMDPTFFFAKCKKFKVMMLK-FGVSVSSVAKSAPEENSEPMTETQ 350
 QY 342 M 342
 Db 351 M 351

RESULT 4
 S63666
 Platelet activating factor receptor mouse

C:Species: Mus musculus (house mouse)
 C:Date: 28-Jul-1996 #sequence_revision 13 Mar-1997 #text_change 28-Jun-2000
 C:Accession: S63666
 R:Shih, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
 Biochem. J. 314: 671-678, 1996

A:Title: A murine platelet activating factor receptor gene: cloning, chromosomal localization
 A:Reference number: S63666; MIM:9629129
 A:Accession: S63666
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-341 <ISH>
 A:Cross-references: EMBL:050872, NID:q125624, PIDD:AA040611, PIR:q1256925
 A:Superfamily: ATP receptor P2U

Query Match 20.6%; Score 366; DB 2; Length 341;
 Best Local Similarity 29.9%; Pred. No. 4, 1e-24;
 Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

QY 20 DKRTIVLFLVLYLVFVGLTNGLAMKIFQI--RKSNTF--TEKNTVISLMLILT 76
 Db 10 DSEFRITLPIVSVIFILGVANGVYLVFAVLEYSKRLNEIKIPVNLIMDLLEFLIT 69
 QY 77 FPKKILSDAKIGCPKTPVQVTSVIFPTWYISISPLGLITIDRYOKTRPKTSNPK 146
 Db 70 LPLMTVY 129
 QY 137 NLGAKIISVIVIAWM-----PLISMLKCPNSATS 321
 Db 130 TRRGKISLILVSIIVAIASVFLATSTNLVYNKDSGNTTGPCHTPIVSVPLIVAV 189
 QY 189 IVVYIVQVITWIMFLI-VIVGYTLITKELRSVPTKRVKVPKRVNKKVITITVPTI 247
 Db 190 FIVCFEFLVFLVFCNVITITLTPMPQO--FRAGV---KRALMVLVTLVAVFI 243
 QY 248 GCVPHFAPVITVTSQFVFCVCAINLTPVYVVESTLMTLSNACIDPFTFELCKSPN 307
 Db 244 GCVPHVYVQVPLVLAELG--YQINPQAIINDALITLTLSTNCVLDPIVYICELTKKPK 301
 QY 308 -----SLISMLKCPNSATS 321
 Db 302 HISEKFSYMSKRSKQ-SRATS 321

RESULT 5
 S43252
 Platelet-activating factor receptor rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Jul-1994 #sequence_revision 13 Nov-1996 #text_change 24-Nov-1999
 C:Accession: S43252
 R:Ridito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.
 Eur. J. Biochem. 221: 21-21R, 1994
 A:Title: Cloning, expression and tissue distribution of rat platelet activating factor
 A:Reference number: S43252; MIM:9422063
 A:Accession: S43252
 A:Molecule type: mRNA
 A:Residues: 1-341 <RIT>
 A:Cross-references: GRI:047400, NID:q470384, PIDD:AAAI84321, PIR:q470385
 A:Superfamily: ATP receptor P2U

Query Match 20.4%; Score 362; DB 2; Length 341;
 Best Local Similarity 28.9%; Pred. No. 9e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

QY 20 DKRTIVLFLVLYLVFVGLTNGLAMKIF--FOIKSKSNFI--PLKNTVISLMLILT 76
 Db 10 DSEFRITLPIVSVIFILGVANGVYLVFAVLEYSKRLNEIKIPVNLIMDLLEFLIT 69
 QY 77 FPKKILSDAKIGCPKTPVQVTSVIFPTWYISISPLGLITIDRYOKTRPKTSNPK 146
 Db 70 LPLMTVY 129
 QY 137 NLGAKIISVIVIAWM-----PLISMLKCPNSATS 321
 Db 130 TRRGKISLILVSIIVAIASVFLATSTNLVYNKDSGNTTGPCHTPIVSVPLIVAV 189
 QY 177 FPKSFGVY 236
 Db 190 FTSCTSPVIFP-----LIVYCMVY 243
 QY 247 KVFITVAVFTGVPFHPAPITPYSQTPVDFVTAENTLEFVEESTLMTLSNACIDP 296
 Db 234 -VCIVIAVY 290
 QY 297 IVPYICKSPN -SLISMLKCPNSATS 321
 Db 291 LYCFELTKKFKHLSSEKFSYMSKRSKQ-SRATS 321

RESULT 6

G protein-coupled receptor 6HL - chicken
 N:Alternate names: purinoceptor 6HL
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
 A:Accession: J04618
 R:Kaplan, M.H.; Smith, D.L.; Sundick, R.S.
 J. Immunol. 151: 628-636, 1993

A:Title: Identification of a G protein-coupled receptor induced in activated T cells.
 A:Reference number: J04618; MIM:94349058
 A:Accession: J04618
 A:Molecule type: mRNA
 A:Residues: 1-308 <KAP>
 A:Cross-references: GRI:06109; NID:q404384; PIDD:AAH05871; PIR:q404384
 R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
 Biochem. Biophys. Res. Commun. 219: 105-110, 1996
 A:Title: Identification of 6HL as a P2Y purinoceptor. P2Y5
 A:Reference number: J04618; MIM:9490677

A:Accession: J04618
 A:Molecule type: mRNA
 A:Residues: 1-308 <WEB>
 A:Cross-references: GRI:06109; NID:q304383; PIDD:AAH065871; PIR:q404384
 A:Experimental source: T-cells
 A:Comment: This receptor plays a role in T-cell activation.
 C:Genetics:

A:Gene: P2Y5
 C:Superfamily: ATP receptor P2U
 C:Keywords: G protein coupled receptor; transmembrane protein
 F:15-40/Domain: transmembrane #status predicted <TM>
 F:51-74/Domain: transmembrane #status predicted <TM>
 F:89-109/Domain: transmembrane #status predicted <TM>
 F:113-157/Domain: transmembrane #status predicted <TM>
 F:177-207/Domain: transmembrane #status predicted <TM>
 F:227-248/Domain: transmembrane #status predicted <TM>
 F:269-292/Domain: transmembrane #status predicted <TM>

Query Match 20.1%; Score 357.5; DB 2; Length 308;
 Best Local Similarity 29.5%; Pred. No. 2e-23;
 Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

QY 14 TSLICRQVKKITQVLPPIALVYLVFVGLTNGLAMKIF--FOIKSKSNFI--PLKNTVISLMLILT 72
 Db 3 SSNCSTELSEKFKTLVGVFSMVY 62

7

111 ELIQUINX IPRKARJSEN, SOMMELI, CYPRIDIN, NESTIKIP (19)

KIMBROUGH, S. K.; TRUMPP, A.; KULTHE, L. M.; KONG, W.; PAYAN, D. G.; HUMNETT, N. W.

Key words: G protein coupled receptor; transmembrane protein

LD 277 QNS - - - JMNINNSVRS - DRTSEVIGAL 323

C:superfamily: vertebrate rhodopsin

89 AMEYKRWIFGNYLCKLASASVSHNLYASVFIITJLSIDRYLAIVHMKSHIKRIMIYAKV] 148

QY 145 SVVIAWFMFLSLPNNILTN RQPRDKNVKCSF LKSEFGLVMEIYNTQ 195
 DB 149 CIIIMLACIASLPIIHNNVFITNTITVCAPHESSNSTLIGLITNNIIS--C- 205
 QY 196 VIFWNLIVIVCYIIITKELKRSVVRIGCVKVRKKVNNKAVPIIIAVFICVPPHA 255
 DB 206 ---FFELLITSTYIMKALKKAVEIQK---NNPRNDITPIIMAVLFFP-----FS 262
 QY 256 RIVYILISQIRGVF-----DCAENTLFFYKESLMTLSINACIDPIFFYFICKSPNS 308
 DB 257 WIPDQIFTFIVLIGQIIISPTGPAIDIVDAMPITITWIAVFNNTINQFVCHICKPKKO 312
 QY 309 LISMK-CENSAISLSQPNK 328
 DB 313 ILQILKYLIPKAKSHSNLSIK 333

RESULT 10

S44425
 angiotensin II receptor type 1 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 19-Mar-1997 #sequence_revision 19 Mar-1997 #text_change 24-Nov-1999
 C:Accession: S44425
 R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
 FEBS Lett. 343, 146-150, 1994
 A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
 A:Reference number: S44425, MIMD:94222188
 A:Accession: S44425
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-359 <DB>
 A:Cross-references: PDB:1AMB30674.1; PID:9546569
 A:Experimental source: liver
 C:Superfamily: vertebrate rhodopsin

Query Match 18.3% Score 326, DB 2, Length 359,
 Best Local Similarity 29.2%, Pred. No. 1.2e 20,
 Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;

QY 26 VLEPLIYVLFVVGILITNGL-AMRIIPQIRSKNPIIFLKNVLSIDLMITPPKILSD 84
 DB 29 VMIFLIVSTIVVATITNSLVVIVFYMKIKTVASVLLNLALDLFLITIPWAVYT 88
 QY 85 AKICGPIKTFVCGVTSVIFFTWYISISPLGLITIDRYOKTTPKTSNKNLGAAIL 144
 DB 89 AMEYRWPFGNYCKIASASVFNIVASVFLIDLSIDRYVALVHMKSHVPRKIMAKVT 148
 QY 145 SVVIAWFMFLSLPNNILTN RQPRDKNVKCSF-----LKSEFGLVMEIYNTQ 195
 DB 149 CIIIMLACIASLPIIHNNVFITNTITVCAPHESSNSTLIGLITNNIIS--C- 205
 QY 196 VIFWNLIVIVCYIIITKELKRSVVRIGCVKVRKKVNNKAVPIIIAVFICVPPHA 255
 DB 206 ---FFELLITSTYIMKALKKAVEIQK---NNPRNDITPIIMAVLFFPSPHPI 258
 QY 255 AKIPIITISQIRGVFICIANITLFFYKESLMTLSINACIDPIFFYFICKSPNS 314
 DB 259 RIVYILISQIRGVF-----DCAENTLFFYKESLMTLSINACIDPIFFYFICKSPNS 318
 QY 315 -CPNSAISLSQPNK 328
 DB 319 YIPDQIFTFIVLIGQIIISPTGPAIDIVDAMPITITWIAVFNNTINQFVCHICKPKKO 333

RESULT 11
 148705
 proteinase activated receptor 2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
 C:Accession: 148705
 R:Nystedt, S.; Larsson, A.K.; Aberq, B.; Sundelin, J.
 J. Biol. Chem. 270, 5950-5955, 1995

A:Title: The mouse proteinase-activated receptor 2 cDNA and protein. Molecular cloning a
 A:Reference number: 148705; MIMD:95157620
 A:Accession: 148705
 A:Status: preliminary, translated from Gh/Gmb/70bJ
 A:Molecule type: mRNA
 A:Residues: 1-399 <DB>
 A:Cross-references: EMBL:248043; NID:9663020; PDB:1AAB9007 1; FII:976021
 C:Superfamily: ATP receptor P2u

Query Match 18.3% Score 325.5, DB 2, Length 399,
 Best Local Similarity 27.6%, Pred. No. 1.5e-20,
 Matches 92; Conservative 74; Mismatches 141; Indels 27; Gaps 12;

QY 22 KIVQVPLIYVLFVVGILITNGL-AMRIIPQIRSKNPIIFLKNVLSIDLMITPPKILSD 80
 DB 74 KITTVYIPVYIIVFVIGLISNMAIMPIIFPKKKKPAVIMANIALADLSIVMIFPK 133
 QY 81 ILSDAKLGIGLRTFVGVQVTSVIFFTWYISISPLGLITIDRYOKTTPKTSNKNLIG 140
 DB 134 ISYHLCNNVYGCALCKVLIGFYGNMYSILPMICLSQRYWVIVNPM-CHPRKKAN 191
 QY 141 AKI-LSVIAWFMFLSLPNNILTN RQPRDKNVKCSF-----LKSEFGLVMEIYNTQ 196
 DB 192 IAVGSLSIIMLILFLVITIPYMKQIYIPA-INTTCHVDEEVLV-GDMFNFLSLA 249
 QY 197 ---VFWNLIVIVCYIIITKELKRSVVRIGCVKVRKKVNNKAVPIIIAVFICVPPHA 254
 DB 250 IGVFLFALLIASAVVIMIKLRSSAMDESEK--KORALRIILIVLAVFICFALSNL 307
 QY 255 AKIPIITISQIRGVFICIANITLFFYKESLMTLSINACIDPIFFYFICKSPNS 313
 DB 308 LIAVHYPLIKV-----KOSHVALIVALCISLNSCIDPEYVYVSKDFRHMARNAL 361
 QY 314 KCPNSAT-----SLSDNKKKEDGDPNRET 340
 DB 362 LTPSVRTVNMQSTLS-SNPKFSKSYSSNST 393

RESULT 12

A48857
 angiotensin II receptor type 1 - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-Dec-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: A48857
 R:Burns, K.D.; Inagami, T.; Harris, R.C.
 Am. J. Physiol. 264, F645-F654, 1993
 A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen
 A:Reference number: A48857; MIMD:93236091
 A:Accession: A48857
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-359 <DB>
 A:Cross-references: GR:559041; NID:9296614; PDB:1AAR2239 1; PID:9499615
 A:Note: Sequence extracted from NCB1 backbone (NCBIN:129600, NCBIPI:129601)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein coupled receptor; transmembrane protein

Query Match 18.3% Score 325, DB 2, Length 359,
 Best Local Similarity 29.2%, Pred. No. 1.5e-20,
 Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;

QY 26 VLEPLIYVLFVVGILITNGL-AMRIIPQIRSKNPIIFLKNVLSIDLMITPPKILSD 84
 DB 29 VMIFLIVSTIVVATITNSLVVIVFYMKIKTVASVLLNLALDLFLITIPWAVYT 88
 QY 85 AKICGPIKTFVCGVTSVIFFTWYISISPLGLITIDRYOKTTPKTSNKNLGAAIL 144
 DB 89 AMEYRWPFGNYCKIASASVFNIVASVFLIDLSIDRYVALVHMKSHVPRKIMAKVT 148
 QY 145 SVVIAWFMFLSLPNNILTN RQPRDKNVKCSF-----LKSEFGLVMEIYNTQ 195

DB 149 CIIIMLALASIAPIHRNVFHEINIIIVCAHYESQNSITIGLIT-KNIIIGPL- 205
 QY 136 VIFWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT-ILAVFIVFPHF 254
 DB 206 -PEPILITSTYLLIMKALKAKEIQR-NKRPENRITFIMAVIIPFSSWHQI 258
 QY 255 AMRYEISQTRIVPCTIAINILEYKESIMLISINAGIDPEIYFELCKSRNLSIMK 314
 DB 256 PEFIVLIVGLAVIIRKRIADIVDIAMPITITICIAVFNNINLEFYGLFKKKKKFELDLK 318
 QY 315 CPNSATSLSDGNRK 328
 DB 319 YIFPKAKSHSNLSIK 333

RESULT 14

p1104

Angiotensin II receptor type 1 human

Accession number: angiotensin II receptor 1A

Species: Homo sapiens (man)

Cloned: Oct 1992 #sequence revision 07-Sep-1997 #text change 21-Jul-2000

Accession: J01104; J01402; J00574; J00574; A44014; S18083

Kobayashi, C.A.; Hwang, C.C.; Fujitani, A.M.; Wu, L.H.; Chang, F.Z.

Biochem Biophys Res Commun 186, 277-284, 1992

A>Title: Cloning, expression, and characterization of a gene encoding the human angioten-

A:Reference number: J01104; M01092337608

A:Accession: J01104

A:Molecule type: DNA

A:Residues: 1-359-370

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

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Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

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Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

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Accession: H01300; J01402; J00574; J00574; J00574

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Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

Accession: H01300; J01402; J00574; J00574; J00574

F:65-90/Domain: transmembrane #status predicted <TM2>
 F:103-124/Domain: transmembrane #status predicted <TM3>
 F:145-167/Domain: transmembrane #status predicted <TM4>
 F:174-210/Domain: transmembrane #status predicted <TM5>
 F:241-264/Domain: transmembrane #status predicted <TM6>
 F:261-305/Domain: transmembrane #status predicted <TM7>
 F:4176-188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.18; Score 321; DB 2; Length 359;

Best Local Similarity 28.78; Pred. No. 3.4e-20;

Matches 92; Conservative 56; Mismatches 139; Indels 34; Gaps 9;

QY 26 VIFWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT-ILAVFIVFPHF 254
 DB 29 VIFWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT-ILAVFIVFPHF 254
 QY 85 AKIQTGPIRIVGVQVSVIYFTMYISISPLGIIIDRYQTRPKYSNPKNLCAKIL 144
 DB 89 AMRYEISQTRIVPCTIAINILEYKESIMLISINAGIDPEIYFELCKSRNLSIMK 314
 QY 145 SVIVIAFVELLSLEKMLIN-FOPEKKNVKKSF-----LKSGLVWHEIVATG 195
 DB 149 CIIIMLALASIAPIHRNVFHEINIIIVCAHYESQNSITIGLIT-KNIIIGPL- 205
 QY 196 VIFWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT-ILAVFIVFPHF 254
 DB 206 -PEPILITSTYLLIMKALKAKEIQR-NKRPENRITFIMAVIIPFSSWHQI 258
 QY 256 KIPYISQTRIVPCTIAINILEYKESIMLISINAGIDPEIYFELCKSRNLSIMK 314
 DB 253 VIFWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT-ILAVFIVFPHF 254
 QY 309 LISMLK-CPNSATSLSDGNRK 328
 DB 313 YIFPKAKSHSNLSIK 333

RESULT 14

J05549

heptahelical P2Y5-like receptor - human

C:Species: Homo sapiens (man)

C:Date: 02-Sep-1997 #sequence revision 05-Sep-1997 #text change 24-Sep-1999

C:Accession: J05549

R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.

Biochem Biophys Res Commun 236, 106-112, 1997

A>Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor

A:Reference number: J05549; M01092336605

A:Accession: J05549

A:Molecule type: DNA

A:Residues: 1-370 <JAN>

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Accession: references: J05549; A0005419; NID:92249034; P109:AM66322.1; P109:AM66322.1

Query Match 18.18; Score 321; DB 2; Length 370;

Best Local Similarity 27.78; Pred. No. 3.4e-20;

Matches 87; Conservative 67; Mismatches 134; Indels 26; Gaps 9;

QY 7 LPSAGNISTKIKYKIIQVLPVLYVIFVGLINGLAMRIE-FOIRKSNFTIFEN 65
 DB 22 LQNALANNI-CLIVDSFKNYINCAVSVVFLIGLINSVSLFVCHMKKRSIAIPIIN 80
 QY 66 TVISDLMLITFPKILSDAKLGTPLETVQVTSVIFFTMYISISPLGIIIDRYQ 125
 DB 81 LAVSDILFVCTIPKIFVFN-RRMPGODHCKISGIAFLINYGSMIFCTISVDFIA 139
 QY 126 TRPKSKSNPKNLCAKILSVIWMFPIISLNNMILINPKPKNNKSSILASPEGL 184
 DB 140 IYFPPSPITIPPRNSALIVAGVMIIVISVSIASLSST-----TNNNAITTCFGLS 195
 QY 185 -VWHEIVATGQVIVWINEIVIVYVITITPELYESVRIE-WKVPKKVKNVKT 214

Job time: 158 sec

DB 194 KRWKLYLSTIIFIEVVGIIPLLNVCSSVRLRKPATLSQIGTN-----KKVY 247
QY 235 NKKVFIIIAVFICFVPEHFAHIIYTHSQRDVEDCAENTLIPYVKSTIMELINACID 294
DB 248 LKMTIVMAFVFCFVNSVLFYALVKSQATINCHLFRPAKIMQTHCLATINCPD 307
QY 295 PTIYFELCKSERNS 308
DB 308 PTIYFELCKSERNS 321

RESULT 15

A42656

angiotensin II receptor type 1B (AT1) - rat

N:Alternate names: angiotensin II receptor chain B

C:Species: Rattus norvegicus (Norway rat)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: A42656; S20423

R:Sandberg, K.; H., H.; Clark, A. T.; Shapiro, H.; Galt, K. J.

J. Biol. Chem. 267, 9455-9458, 1992

A:Title: Cloning and expression of a novel angiotensin II receptor subtype.

A:Reference number: A42656; M01D:92250585

A:Accession: A42656

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <SAS>

A:Cross-references: GR:M00065; NID:q202801; PDB:AAA40704.1; PDB:q202802

A:Experimental source: adrenal cortex

A:Note: sequence extracted from NCH1 backbone (NCH1N:100262, NCH1P:100268)

R:Wai, N.; Inagami, T.

FEBS Lett. 298, 257-260, 1992

A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.

A:Reference number: S20423 M01D:92183879

A:Accession: S20423

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <TMA>

A:Cross-references: GB:X64052; NID:q57521; PDB:GMA45410.1; PDB:q57522

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.9%; Score 319; DB 2; Length 359;

Best Local Similarity 29.68; Pred. No. 4.9e-20;

Matches 92; Conservative 54; Mismatches 137; Indels 28; Gaps 10;

QY 26 VLPLIATVLEFVGLIINCL-AMRIPOIRSKSNFIIFLKNIVISDILMIITPPFKIISD 84
DB 29 VMPTLESIIFVVGIFGNSLVIVIFYMKLIVASVELLNLALADLCFLILPLMAVYT 88
QY 85 AKIQTGILRTFVCOVTSVIFFTMYISIPILGILITIDRYOCTTRPKISNPKNIIQAKIL 144
DB 89 AMFYRWPFGNHICKIASASVSFNIVASVPLITCISIDRYLAIVHPKSRIRRTMLVAKYV 148
QY 145 SVVIMAFMPLISTPNMILTNRO-PRKNVKKSF-----LKSEGLWHEIVNYIQ 195
DB 149 CIIIMLMAGIASIPAVIRNVYFIENTNITVCAHYRSONSTLPICGLIT-KNIIQFV-- 205
QY 196 VIFWIMFLIVICVTLLIKELYSVYRQGVKPKKRVNKKV-11IAV--FPICFVP 251
DB 206 ----FPLIILITSTYLIMKALKKAYKTK--NTPR---NDIFRITIMAVLEFFESWVP 255
QY 252 PHEAKIITYTISQTDVDCITAEHTLIPYVKSTIMLTSIACIDDPITYFELCKSERNSIS 311
DB 256 HQIPTFDVILQIGIIRKCEIADIVIPAMPTTICIAVFNNCLNIPFGYGLCKKKKKYPIQ 315
QY 312 MLK-CPNSATS 321
DB 316 LKVIPTPAKS 326

Search completed: August 21, 2002, 15:45:46



GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2002, 15:44:03 : Search time 28.98 Seconds

(without alignments)
2041.555 Million cell updates/sec

Title: US-09-780-576-2
Perfect score: 1778
Sequence: 1 M04VDNI:USAGNLSICTRP

SQNNPKKKGQVWQVNPFFPM 342

Scoring table: BLOSUM62
Gapop 10.0 Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:viirus:*
16: SP:bacteriophage:*
17: SP:archaea:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	4	Q9H244
2	1748	98.3	342	6	Q9BGT8
3	1748	98.3	342	6	Q9BGT8
4	1555.5	87.5	347	11	Q9CPV9
5	1528.5	86.0	343	11	Q9CPV9
6	829	46.6	333	4	Q9BPV8
7	794	44.7	337	11	Q9BGT8
8	741.5	41.7	348	11	Q9BGT8
9	699.5	39.3	358	4	Q9BGT8
10	694.5	39.1	358	4	Q9BGT8
11	685.5	38.6	359	11	Q9BGT8
12	559	31.4	228	6	Q9BGT8
13	553.5	31.1	269	4	Q9BGT8
14	448	25.2	176	4	Q9BGT8
15	388.5	21.9	342	6	Q9BGT8
16	387.5	21.8	342	6	Q9BGT8

17	368.5	20.7	296	6	Q9TY6	Q9TY6 canis fami
18	367	20.6	345	6	Q9BGT8	Q9BGT8 sus scrofa
19	365	20.5	342	6	Q9BGT8	Q9BGT8 sus scrofa
20	356	20.0	374	13	Q9BGT8	Q9BGT8 sus scrofa
21	347.5	19.5	330	4	Q9BGT8	Q9BGT8 sus scrofa
22	347.5	19.5	346	4	Q9BGT8	Q9BGT8 sus scrofa
23	344	19.3	309	11	Q9BGT8	Q9BGT8 sus scrofa
24	343	19.3	359	13	Q9BGT8	Q9BGT8 sus scrofa
25	339.5	19.1	309	11	Q9BGT8	Q9BGT8 sus scrofa
26	338	19.0	359	6	Q9BGT8	Q9BGT8 sus scrofa
27	334	18.8	367	4	Q9BGT8	Q9BGT8 sus scrofa
28	328	18.4	340	6	Q9BGT8	Q9BGT8 sus scrofa
29	322	18.1	359	11	Q9BGT8	Q9BGT8 sus scrofa
30	321	18.1	359	6	Q9BGT8	Q9BGT8 sus scrofa
31	318	17.9	361	11	Q9BGT8	Q9BGT8 sus scrofa
32	316	17.8	377	11	Q9BGT8	Q9BGT8 sus scrofa
33	314	17.7	400	6	Q9BGT8	Q9BGT8 sus scrofa
34	311	17.5	361	11	Q9BGT8	Q9BGT8 sus scrofa
35	309.5	17.4	298	4	Q9BGT8	Q9BGT8 sus scrofa
36	309.5	17.4	339	11	Q9BGT8	Q9BGT8 sus scrofa
37	309	17.4	358	13	Q9BGT8	Q9BGT8 sus scrofa
38	309	17.4	454	4	Q9BGT8	Q9BGT8 sus scrofa
39	308	17.3	400	6	Q9BGT8	Q9BGT8 sus scrofa
40	307	17.3	359	11	Q9BGT8	Q9BGT8 sus scrofa
41	304.5	17.1	339	11	Q9BGT8	Q9BGT8 sus scrofa
42	304.5	17.1	352	11	Q9BGT8	Q9BGT8 sus scrofa
43	304.5	17.1	393	11	Q9BGT8	Q9BGT8 sus scrofa
44	304.5	17.1	401	11	Q9BGT8	Q9BGT8 sus scrofa
45	304.5	17.1	438	11	Q9BGT8	Q9BGT8 sus scrofa

ALIGNMENTS

RESULT	ID	PRELIMINARY	FR	342 AA
Q9H244	Q9H244	PRELIMINARY	FR	342 AA
AC	Q9H244	Q9H244		
DT	01-MAR-2001	(TREMBLrel, 16, Created)		
DT	01-MAR-2001	(TREMBLrel, 16, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)		
DE	P2112 PLATELET ADP RECEPTOR (G-PROTEIN COUPLED RECEPTOR SPI999)			
GN	(G1-COUPLED ADP RECEPTOR HOKR3)			
OS	HOKR3			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-21037966; PubMed-1196645;			
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,			
RA	Panakrishnan V., Yang P.-B., Nudsen P., Nudsen A., Julius D.,			
RA	Conley P.H.,			
RI	"Identification of the Platelet ADP Receptor Targeted by			
RT	Antithrombotic Drugs."			
RL	Nature 409:202-207(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-21269433; PubMed-1194774;			
RA	Zhang F.L., Luo L., Gustafson W., Jacobowitz J., Smith M., Zhao X.,			
RA	Lin Y.-H., Chen G., Pramank H., Jaz T.M., Palmer K., Hayne M.,			
RA	Monsma F.J., Jr.,			
RT	"ADP Is the cognate ligand for the orphan G protein-coupled receptor			
RI	SP1999."			
RL	J Biol Chem 276:8608-8615(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-2141281; PubMed-11502873;			
RA	Takasaki T., Kanohara M., Saito T., Matsuno M., Matsuno S.,			
RA	Ohishi T., Soga T., Matsushima H., Furutachi K.,			
RT	"Molecular cloning of the platelet p21ac ADP receptor:"			
RI	Pharmacological comparison with another ADP receptor, the p2Y1			

61	receptor	603432.439(2001)	
62	Mol. Pharmacol.	603432.439(2001)	
63	EMBL	AF414449; AAC08944.1	
64	EMBL	AF418155; AAC00948.1	
65	EMBL	AB052684; BAB0824.1	
66	GenBank	U9800276; GPCR_human	
67	PIR	P00001; 7fm.1	
68	PIR	P00001; GPCR_HUMAN	
69	PROSITE	PS50262; G_PROTEIN_RECEP_F1_2	1
70	SEQUENCE	442 AA	99438 MW: 85540274.66891765 CRO64

[illegible]

RESULT	2			
ID	Q9BCTH	PRELIMINARY:	PRG:	342 AA.
AC	Q9BCTH			
DT	01-JUN-2001	(TREMBLrel. 17, created)		
DI	01-JUN-2001	(TREMBLrel. 17, last sequence update)		
DR	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	HYPOPHYSICAL, 49.5 KDa PROTEIN.			
OS	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;			
OG	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OX	NCBI TaxID: 95411			
RA	[1]			
RF	SEQUENCE FROM N.A.			
RG	TISSUE: FRONTAL LOBE LEFT.			
RA	Osada N., Hida M., Kusuda T., Tanuma F., Iseki K., Hirai M., Terao K.,			
RA	Suzuki Y., Sogano S., Hashimoto K.?			
RI	Isolation of full length cDNA clones from macaque brain cDNA			
RI	libraries.?			
RL	SUBMITTED (FEV 2001) to the EMBL/GenBank/DDBJ databases			
DR	EMBL: AB076485; BA040411;?			
DR	InterPro: IPR000276; GPCR_Rhodopsin.			
DR	PIR: P400001; Trm_1_1.			
DR	PRINTS: PR00247; GPCR_Rhodopsin.			
DR	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.			
DR	Hypothetical protein.			
SC	SEQUENCE: 342 AA; 49497 MW; 4021BF987FC48599 CH664;			

Best Local Similarity 98.08; pred. No. 1,66-148;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY	1	MOA	NI	SA	GN	SI	CT	RO	KK	IV	PE	LT	VT	FA	GL	LT	NI	AM	IF	QJ	PS	KS	NI	60							
Dh	1	MOA	NI	SA <td>GN<td>SI<td>CT<td>RO<td>KK<td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	GN <td>SI<td>CT<td>RO<td>KK<td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	SI <td>CT<td>RO<td>KK<td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	CT <td>RO<td>KK<td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	RO <td>KK<td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td>	KK <td>IV<td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td></td>	IV <td>PE<td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td></td>	PE <td>LT<td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td></td>	LT <td>VT<td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td></td>	VT <td>FA<td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td></td>	FA <td>GL<td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td></td>	GL <td>LT<td>NI</td><td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td></td>	LT <td>NI</td> <td>AM<td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td></td>	NI	AM <td>IF<td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td></td>	IF <td>QJ<td>PS<td>KS<td>NI</td><td>60</td></td></td></td>	QJ <td>PS<td>KS<td>NI</td><td>60</td></td></td>	PS <td>KS<td>NI</td><td>60</td></td>	KS <td>NI</td> <td>60</td>	NI	60							
QY	61	IF	KN	VI	SD	LM	LT	EP	PK	IL	SL	AK	IG	CP	RI	VC	QV	SV	IF	ET	MY	SI	SP	IG	LT	120					
Dh	61	IF	KN	VI	SD	LM	LT	EP	PK	IL	SL	AK	IG	CP	RI	VC	QV	SV	IF	ET	MY	SI	SP	IG	LT	120					
QY	121	DR	OK	TR	PE	KT	SN	RK	NI	U	AK	IS	SV	IA	MP	IL	SI	KN	ML	IN	OP	OR	KK	SV	KS	SP	KS	180			
Dh	121	DR	OK	TR	PE	KT	SN	RK	NI	U	AK	IS	SV	IA	MP	IL	SI	KN	ML	IN	OP	OR	KK	SV	KS	SP	KS	180			
QY	181	FF	SL	VM	HE	IV	NY	IC	OV	IP	NI	FL	IV	NY	YT	LT	FE	EL	VS	YT	PO	VS	VP	PK	NY	VE	Y	240			
Dh	181	FF	SL	VM	HE	IV	NY	IC	OV	IP	NI	FL	IV	NY	YT	LT	FE	EL	VS	YT	PO	VS	VP	PK	NY	VE	Y	240			
QY	241	IA	VE	FE	IC	VE	PE	HE	IV	NY	YT	LT	FE	EL	VS	YT	PO	VS	VP	PK	NY	VE	Y	240							
Dh	241	IA	VE	FE	IC	VE	PE	HE	IV	NY	YT	LT	FE	EL	VS	YT	PO	VS	VP	PK	NY	VE	Y	240							
QY	301	IC	KS	PR	NS	LS	SM	K	C	P	N	S	A	T	S	I	S	O	N	R	K	K	B	O	G	P	N	E	ET	TM	342
Dh	301	IC	KS	PR	NS	LS	SM	K	C	P	N	S	A	T	S	I	S	O	N	R	K	K	B	O	G	P	N	E	ET	TM	342

RESULT	3			
U95KC3	1D	Q95KC3	PRELIMINARY;	PRF; 342 AA.
AC	Q95KC3			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	HYPOTHETICAL, 39.5 KDA PROTEIN.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).			
OC	Eukaryota; Metazoa; Chordata; Ctenata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_Taxid=9541;			
RN	[1]			
RP	SOURCE: FROM N.A.			
RC	TISSUE: MEDULLA OBLONGATA;			
RA	Osada N., Hida M., Kusuda J., Tanuma F., Iseki K., Hirai M., Terao K.,			
RA	Suzuki Y., Sugano S., Hashimoto K.;			
RT	"Isolation of full-length cDNA clones from macaque brain cDNA			
RT	libraries.";			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AH062981; BAB60747.1; -			
KM	Hypocretinal protein.			
UN	SEQUENCE 342 AA; 39479 MW; E93FC26BFF5EC4C CRD54;			

Query Match	98.38	Score 1748	DB 6	Length 342
Host Local Similarity	98.08	Prod. No. 1.6e-148		
Matches 335	Conservative	3	Mismatches 4	Indels 0
			Gaps	0
QY	1	MOAVDLNLSAGNLSLTCTDPRKLTQVLEPFLLYALFEVGLITNLSLAMEFPDIPKSKNFI	60	
	1			
Db	1	MOADLNLSAGNLSLTCTDPRKLTQVLEPFLLYALFEVGLITNLSLAMEFPDIPKSKNFI	60	
QY	61	TEKNNTVSLDMLITTFPRKLTSDAKLTSGELKHYVGVTVVITFYMYNISTSLGLTTI	120	
	1			
Db	61	TEKNNTVSLDMLITTFPRKLTSDAKLTSGELKHYVGVTVVITFYMYNISTSLGLTTI	120	
QY	121	DRYQKTRPFTSNPKNLGAKLISVVAWAFMPLISLIDNMLIFNKQDPRDKKVVKKCSFLKS	180	
	1			
Db	121	DRYQKTRPFTSNPKNLGAKLISVVAWAFMPLISLIDNMLIFNKQDPRDKKVVKKCSFLKS	180	
QY	181	EEGLVMEHETVYTCQVLTWINEFLVLYVYTLTETELRSYPTKRVGVGPKKKNVKKYFI	240	
	1			
Db	181	EEGLVMEHETVYTCQVLTWINEFLVLYVYTLTETELRSYPTKRVGVGPKKKNVKKYFI	240	

OY 241 11AVFICVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 300
 DB 241 11AVFICVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 300
 OY 301 11KSPFNSTLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 342
 DB 301 11KSPFNSTLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 342

RESULT 4
 OYCPV9 PRELIMINARY: PRT: 347 AA.

AC 09CIV9;
 DT 01-JUN-2001 (TEMBLrel, 17, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel, 19, Last annotation update)
 DE 492150123RIK PROTEIN (29000796228K, protein)
 GN P2RY12 OR 4921504123RIK OR 29000796228K
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;

SEQUENCE FROM N.A.
 STRAIN-657H/61; TISSUE=TESTIS, AND HIPPOCAMPUS;
 MEDLINE-21085660; PubMed-11217851;
 RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
 Saito T., Ozazaki Y., Gotohori T., Hono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Hatalov S., Casavant T.,
 Felschmann W., Gaasterland T., Glasi C., King B., Kothliw H.,
 Schmil P., Lewis S., Matsuo Y., Nikaide T., Pesole G., Quackenbush J.,
 Schmitt L.M., Staudt R., Suzuki R., Tomita M., Wanner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Harsh G.,
 Blake J., Botfield D., Hayano M., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
 Gustimich S., Hill D., Helmann M., Hume D.A., Kamaya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Membraris P.,
 Nordone P., Rind B., Ringwald M., Rodriguez T., Sakamoto N.,
 Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 Hayashizaki Y.
 RA Functional annotation of a full-length mouse cDNA collection.
 RT Nature 409:685-690(2001).
 RL EMBL: AK014807; BAR29561.1;
 DR EMBL: AK014807; BAR29561.1;
 DR MGI: 1918089; P2RY12.
 DR MGI: 1920408; 29000796228K.
 DR InterPro: IPR000276; GPCR_Protein
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCR_HOMOPOSN.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SO SEQUENCE 347 AA; 39473 MW; P107488B57E025F1 CCK64;

Query Match 87.5%; Score 1555.5; DB 11; Length 347;
 Best Local Similarity 88.7%; Pred No 2,7e-131;
 Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;
 OY 6 N1LSAFCNTSLCTRDYKITTQVLLFLLVTVLFFVCGIINGLAMPPIPOQPSKSNFTIFLKN 65
 DB 12 N1LSAFCNTSLCTRDYKITTQVLLFLLVTVLFFVCGIINGLAMPPIPOQPSKSNFTIFLKN 71
 OY 66 TVISDLMLITPPPKILISAKLIGTGLRPPVCGVTSVIFVFTWYISISFGLITIDRYOK 125
 DB 72 TVISDLMLITPPPKILISAKLIGTGLRPPVCGVTSVIFVFTWYISISFGLITIDRYOK 131
 OY 126 TTRPKTSNPKNLGAKLISVIVAWFMFLISLPMNMLTRORPKKVKCSFLKSEGLV 185
 DB 132 TTRPKTSNPKNLGAKLISVIVAWFMFLISLPMNMLTRORPKKVKCSFLKSEGLV 191

OY 186 WHEIVNYICQVIFWIFNIFLIVCVTLITKELYSRVTRGCVPRKKVNVKVF11AAV 245
 DB 192 WHEIVNYICQVIFWIFNIFLIVCVTLITKELYSRVTRGCVPRKKVNVKVF11AAV 251
 OY 246 FICFVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 305
 DB 252 FICFVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 311
 OY 306 RNSLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 342
 DB 312 RNSLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 347

RESULT 5
 OYCPV9 PRELIMINARY: PRT: 343 AA.

AC 09EPX4;
 DT 01-MAR-2001 (TEMBLrel, 16, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel, 17, Last annotation update)
 DE P2RY12 PLATELET ADP RECEPTOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
 Saito T., Ozazaki Y., Gotohori T., Hono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Hatalov S., Casavant T.,
 Felschmann W., Gaasterland T., Glasi C., King B., Kothliw H.,
 Schmil P., Lewis S., Matsuo Y., Nikaide T., Pesole G., Quackenbush J.,
 Schmitt L.M., Staudt R., Suzuki R., Tomita M., Wanner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Harsh G.,
 Blake J., Botfield D., Hayano M., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
 Gustimich S., Hill D., Helmann M., Hume D.A., Kamaya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Membraris P.,
 Nordone P., Rind B., Ringwald M., Rodriguez T., Sakamoto N.,
 Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 Hayashizaki Y.
 RA Functional annotation of the platelet ADP Receptor Targeted by
 RT Anticubulinic Drugs.
 RT Nature 409:202-207(2001).
 RL EMBL: AF134503; AAC48945.1;
 DR InterPro: IPR000276; GPCR_Protein
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCR_HOMOPOSN.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 SO SEQUENCE 343 AA; 39047 MW; 7AF04VCH66674136 CCK64;

Query Match 86.0%; Score 1528.5; DB 11; Length 343;
 Best Local Similarity 86.9%; Pred No 6,9e-129;
 Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;
 OY 6 N1LSAFCNTSLCTRDYKITTQVLLFLLVTVLFFVCGIINGLAMPPIPOQPSKSNFTIFLKN 65
 DB 12 N1LSAFCNTSLCTRDYKITTQVLLFLLVTVLFFVCGIINGLAMPPIPOQPSKSNFTIFLKN 71
 OY 66 TVISDLMLITPPPKILISAKLIGTGLRPPVCGVTSVIFVFTWYISISFGLITIDRYOK 125
 DB 72 TVISDLMLITPPPKILISAKLIGTGLRPPVCGVTSVIFVFTWYISISFGLITIDRYOK 131
 OY 126 TTRPKTSNPKNLGAKLISVIVAWFMFLISLPMNMLTRORPKKVKCSFLKSEGLV 185
 DB 132 TTRPKTSNPKNLGAKLISVIVAWFMFLISLPMNMLTRORPKKVKCSFLKSEGLV 191
 OY 186 WHEIVNYICQVIFWIFNIFLIVCVTLITKELYSRVTRGCVPRKKVNVKVF11AAV 245
 DB 192 WHEIVNYICQVIFWIFNIFLIVCVTLITKELYSRVTRGCVPRKKVNVKVF11AAV 251
 OY 246 FICFVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 305
 DB 252 FICFVPHFARIPYTLISOTRDVFDCAENTLFFVKESTLMLSLNACLDPPITYFF 311
 OY 306 RNSLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 342
 DB 312 RNSLSMLKCPNSATSLSDNRRKKKQDGGDPPNEETPM 343

[illegible]

QY 197 IFWIFNFIIVGVIIITKELYSVYRRCVGVAPKKVNVVHIIIVAFVCHVPEEAR 256
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 195 IEFVVFILMLFEVYVIAKKKYDYSRKSCKDKRNNKKLEGVFVAVVFTVCFAPHEAR 254
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 257 IPTVLSQTRVDFVDTAANIIEYVKRSTIMVLSNATLDFVTFPLGCSFKSNLSMLKDP 316
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 255 VPIYHSSTQNRKTKIQLQNIIFIAKFTFLPLAATINIMPLILYIFLCKKFLIKLQMW-IG 312
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 317 NSATSLSDQNRKKKQD 332
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 313 KKTIASSQENHSSQITD 328
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 RESULT 7 PRELIMINARY: PRT: 337 AA.
 Q9D812
 AC Q9D812;
 DT 01-JUN-2001 (TREMblrel, 17, Created)
 DT 01-JUN-2001 (TREMblrel, 17, last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, last annotation update)
 DE 2010001L06PIK PROTEIN.
 GN GPP86 OR 2010001L06PIK.
 OS Mus musculus (Mouse).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
 CC Mammalia, Eutheria, Rodentia, Scuriognathi, Muridae, Murinae, Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:G57H1/6J; TISSUE:SMALL INTESTINE;
 RX MEDLINE:21085660; PUBMED:11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa K., Izawa A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka S.,
 Saito T., Okazaki Y., Gyojopori T., Iono H., Kasaiyawa T., Saito R.,
 Kaku K., Matsuda H.A., Ashburner M., Balow S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schirral L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sasaki K., Okido T., Furuno M., Aono H., Raddarrelli P., Parish G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
 Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli F., Mombauts P.,
 Nordup P., Ping B., Pinwald M., Rodriguez I., Sakamoto N.,
 Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 Suzuki H., Toyokawa K., Wang K.H., Wells C., Whitaker G., Wilming L.,
 Wyszynski A., Yoshida K., Yasugawa Y., Kawaji H., Kohsaki S.,
 Hayashizaki Y.;
 KA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008013; BAB25409.1;
 DR MGD: MG1:1921441; GCF86.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF000801; 7tm.1.1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN-RECEP.F.1.; UNKNOWN.1.
 DR PROSITE: PS50262; G-PROTEIN-RECEP.F.2.1.
 DP SEQUENCE 337 AA: 38693 MW: 201467BFB93D5EA CR:64;
 Query Match 44.7%; Score 794; DH 11; Length 337;
 Best Local Similarity 45.9%; Pred. No. 3, 2e-63;
 Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps
 QY 6 NLSAPG-NFSLCTDRKRTGVLPFLVTVLFEVGLITNCLAMKIFFGKRSNFIPL 64
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 6 NTTCQGFENKSRGCRPRDPMKQILFEVYITVYVFLAGLITNVALVAVHILPNSNFIYVI 65
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 64 KNYVSDLMILTFPRKILSDAKLGTPRTFVGVTVYTFYTFYTFYISFLGLITIDR 124
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 66 KNTIVADILMALMIPKILSDSHLAWQIGCVYGLSSVYVFTMYVGMIMLQILAVDR 125
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 124 QRTREPKTSNPKLLGAKILSVIWMFLLSLPNNMLTNRQPROKVKKCSFLKSEFG 183
 ID 126 LKIMPEKRTIAFAIVASISWMSLMPFLSLPNNML-NKELTPSSVKKCKASLSPILG 184
 QY 184 LVMHPIVAVICGVIVWINEIIVCYTLITREKHSVYRTGKGVKKVKKVAVI111A 243
 DB 185 LAMHGVVSHITCOLITMAVILMLLEFVAVITKVKVSKRPSKDS-PHKKLEFVAVI11A 243
 QY 244 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 303
 DB 244 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 303
 QY 304 SFERNLSLMLKCPNSATSLSDNKKKEOP 332
 DB 304 KFTQKVCVWCKAKRTAGSSRHHSSQTD 332

RESULT 8
 Q96J28 PRELIMINARY: PRT: 338 AA.
 ID Q96J28
 AC 01-MAR-2001 (TREMblrel, 16, Created)
 DT 01-MAR-2001 (TREMblrel, 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel, 17, Last annotation update)
 DE 7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee B.C., Stradden D.T.:
 RT 7 Transmembrane G protein coupled receptor from hematopoietic
 RT precursors.
 RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF177211; AAC09275.1;
 DR InterPro: IPR000276; GPCR-Rhodopsin.
 DR Pfam: PF00601.7; 1.
 DR PRINTS: PR00247; GPCRHHODOPSN.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL2; 1.
 DR Receptor: Transmembrane.
 KW SEQUENCE 338 AA: 38861 MW: 4376506226884E GR64;

Query Match 41.7%; Score 741.5; DB 11; Length 338;
 Best Local Similarity 44.1%; Pred No 16e-58;
 Matches 146; Conservative 69; Mismatches 109; Indels 7; Gaps 3;

QY 4 VDNLTAPNTSLCTRTYKITOVLEPLLYTLFFVGLITNGLARIFQLSKSNFIIFL 63
 DB 1 MNSSTIDPPNCPGWNNTLITKQITIVYGVVFTICLLNGISCMIPFVIVSSKSPIT1YL 60
 QY 64 KNIVISDLMLITPEPKILSDAKIGTGPITRFVQVTSVTFYFWYISISPLGLITIDRY 123
 DB 61 KNIVAVFLMLITPEPKVLDNSISLPMQVNECVASVIEFVNVYISVEFGISPDY 120
 QY 124 QRTREPKTSNPKLLGAKILSVIWMFLLSLPNNMLTNRQPROKVKKCSFLKSEFG 183
 DB 121 YKIVKPLITISVSVANSKLSVIMMLLAVPNIITLNGCKVEVKIQCMEIKNGLG 180
 QY 184 LVMHPIVAVICGVIVWINEIIVCYTLITREKHSVYRTGKGVKKVKKVAVI111A 243
 DB 181 KKHMKASNYIPVSIPIWVVFLLILVFTALITRKIFKSHIKSRKNSISVKKSSRNIPSVI 240
 QY 244 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 303
 DB 241 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 300
 QY 304 SFERNLSLMLKCPNSATSLSDNKKKE 330
 DB 301 PFRKYLAKKIMSLKYN--DLFVSKTKR 328

RESULT 9
 Q96J28 PRELIMINARY: PRT: 358 AA.
 ID Q96J28
 AC 01-DEC-2001 (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
 DE CDNA FLJ14878.1; Clone F14878.1; WEAKLY SIMILAR TO PROBABLE
 DE G-PROTEIN-COUPLED RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-PLACENTA;
 RA Isogai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Watanabe S., Hosofuji T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
 RA Niromiya K., Iwayanagi T.;
 RT "NEO Human cDNA sequencing project."
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027784; BAB5366.1;
 DR SEQUENCE 358 AA: 41462 MW: 782270068900779 GR64;

Query Match 39.3%; Score 699.5; DB 4; Length 358;
 Best Local Similarity 42.6%; Pred No 9.6e-55;
 Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

QY 6 NITSANG-NISICTRYKITOVLEPLLYTLFFVGLITNGLARIFQLSKSNFIIFL 64
 DB 25 NISDGLMLITPEPKILSDAKIGTGPITRFVQVTSVTFYFWYISISPLGLITIDRY 124
 QY 65 NTVISDLMLITPEPKILSDAKIGTGPITRFVQVTSVTFYFWYISISPLGLITIDRY 124
 DB 82 NIYVADLMLITPEPKILSDAKIGTGPITRFVQVTSVTFYFWYISISPLGLITIDRY 141
 QY 125 KTRPEKTSNPKLLGAKILSVIWMFLLSLPNNMLTNRQPROKVKKCSFLKSEFG 184
 DB 142 KVVAFPGDSRMVNTITFTKVLSCVWIMVAVLSPLITLNGOPTEDNIDHCKSLKSPILG 201
 QY 185 VMLHPIVAVICGVIVWINEIIVCYTLITREKHSVYRTGKGVKKVKKVAVI111A 243
 DB 202 KMHAVIYVNSCLFVAVLITLIGYTAISRYIKS-SFGFTSQSSRPRTNOSTRVAVA 259
 QY 244 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 303
 DB 260 VFFICVPHFARIPYTLISQTRVDICAKNTLFFVKKESITMLTSLNACLDPPITFFI1CK 319
 QY 304 SFERNLSLMLKCPNSATSLSDNKKKE 330
 DB 320 SFERNLSLMLKCPNSATSLSDNKKKE 348
 RESULT 10
 Q96J21 PRELIMINARY: PRT: 358 AA.
 ID Q96J21
 AC 01-JUN-2001 (TREMblrel, 17, Created)
 DT 01-JUN-2001 (TREMblrel, 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
 DE G-PROTEIN-COUPLED RECEPTOR 87.
 GN GPR47 (GPR45).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match: 39.1%; Score 694.5; DB 4; Length 356;
 Best Local Similarity: 42.2%; Pred. No. 2.7e 54;
 Matches: 159; Conservative: 68; Mismatches: 113; Indels: 9; Gaps: 5

CSHL 11	PRELIMINARY;	PRT;	359	AA
99MT7				
099MT7				

Wittendorfer T., Schaller H.C., Holtebrand S.: "An expressed sequence tag (EST) data mining strategy succeeding in

Query Match	38.6%;	Score 685.5;	DB 11;	Length 359;
Best Local Similarity	41.7%;	Pred. No. 1.7e-53;		
Matches 136;	Conservative 65;	Mismatches 120;	Indels 5;	Gaps 4;

RESULT	12		
09BE53			
09BE53			
PRELIMINARY;			
PRT;	228	AA	

PROSITE: PS00247 G_PROTEIN_RECEP_F1_1 UNKNOWN_1
PROSITE: PS02622 G_PROTEIN_RECEP_F1_2 1
SEQUENCE 228 AA; 26356 MW; 47907F5040H00220C CRG64

Query Match	31.48;	Score 559;	DB 6;	Length 228;
Best Local Similarity	46.78;	Prod No 2 2e-42;		
Matches 105;	Conservative 40;	Mismatches 78;	Indels 2;	Gaps 1

[illegible]

RESULT 13

1D	Q9HXC2	PRELIMINARY;	PRT;	269	AA.
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DT 01-JUN-2001 (TEMBREL, 17, Created)
 DT 01-JUN-2001 (TEMBREL, 17, Last sequence update)
 DT 01-DEC-2001 (TEMBREL, 19, Last annotation update)
 DE POTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG78 (G-PROTEIN-COUPLED RECEPTOR
 DE 87).
 DE FKSG78.
 GN Homo sapiens (Human).
 OS
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eultheria; Primates; Catarrhini; Hominidae; Homin.
 CX NCBI_taxid=9606;
 KN [1]
 KN SP SOURCE FROM N A
 KN RC
 KN TISSUE=HEART;
 RA Wang Y.-Y, Gong L.;
 FT Identification of FKSG78, a novel gene encoding a putative G-protein-
 FT coupled receptor.
 RT Submitted (Feb-2001) to the EMBL/GenBank/DDBJ databases.
 KN [2]
 KN SEQUENCE FROM N A.
 RP TISSUE=LONG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
 RC Strausberg R.;
 RA Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 RL -1. SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DE EMBL: AF345566; AK220069.1.
 DE EMBL: BC009540; AA009540.1; -.
 DR InterPro: IPR000276, GPCR_Foldpsn
 DR Pfam: PF00001, 7tm_1, 1.
 DR PRINTS: PR00237, GPCRHH002N.
 DR PROSITE: PS00237, G-PROTEIN_RECEP_FL_1, 1.
 DR PROSITE: PS00262, G-PROTEIN_RECEP_FL_2, 1.
 G-protein coupled receptor, glycoprotein, Receptor, Transmembrane
 SEQUENCE 269 AA: 1444 MW: 167049EE2071776 rnc64.

Query Match	31.18;	Score 553.5;	DH 4;	Length 269;
Best Local Similarity	42.58;	Pred. No. 8.2e-42;		
Matches 11;	Conservative 50;	Mismatches 95;	Indels 5;	Gaps 3

[illegible]

QY	193	ICQVLEFIMNPLIIVCIVCILLIKELIKELISVVRITRQGGKVIHK-KANVAKVFIILAVPEICFVP	264
Db	111	VNSTLEFVAVITTTNCTYATATFYTHK--SSTGTSLSNPFRRHDSIFVAVAVITTTT	178
QY	252	EHFARFVLTSLQKDFVETAEITLFTVKESTLMLISLNLCLDFEYFIFKFKRNSLI-	310
Db	179	YHICLIPPTFSLDLRLADESAQKIIHYCKELITLTSACNVCLDFIYTFHMKKSFSSKRLFK	248
QY	311	SMKQPNSTATSLQDNRRKE	340
Db	239	KSNITPFSSTPLSLQSVPPSE	259

RESULT 14

ID	Q9BY61	PRELIMINARY;	PRT;	176 AA
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LT 01-JUN-2001 (TEEMHIREL_17, Created)
 DT 01-JUN-2001 (TEEMHIREL_17, last sequence update)
 DT 01 DEC 2001 (TEEMHIREL_19, last annotation update)
 DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPCR.
 OS Homo sapiens (human).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
 CC Mammalia; Plithozoa; Primates; Carnivora; Eumetazoa; Hemichordata; Chordata.
 CX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Zhang W., Mao T., Cao X.:
 RT "Molecular cloning of a probable G protein-coupled receptor with three
 transmembrane domains."
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF178982; AAK18752.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; Tm1.1; 1.
 DR PRINTS: FF00237; GPCRHOOPSN.
 DR PROSITE: PS50262; G_PROTEIN_RKCP_F1_2; 1.
 KW Receptor.
 SQ SOURCE: 176 AA; 20194 MW; 352PDA2EA70EF9AD CRC64;

Query Match	25.28	Score 448	DB 4	Length 176
Best Local Similarity	46.88	Prod. NO. 1.5e-32		
Matches	81	Conservative	33	Mismatches 57
			Indels	2
			Gaps	1

[illegible]

RESULT	15
Q9TYE	

1D	0911195	PRELIMINARY;	342 AA
AC	0911195:	PRF;	

DT 01 MAY 2000 (TREMREL, 13, Created)
 DT 01 MAR 2001 (TREMREL, 16, Last sequence update)
 DT 01-DEC-2001 (TREMREL, 19, Last annotation update)
 DE PLATELET-ACTIVATING FACTOR RECEPTOR.
 CN PAIR.
 CS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Artiodactyla; Ruminantia; Bovidae; Bovulidae.
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovulidae.
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN 111
 RP SEQUENCE FROM N.A.

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 21, 2002, 15:44:28, Search time: 13.43 Seconds
(without alignments) 986 008 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778
Sequence: 1 MOAVDPNLTSAQNTSLCTPD

SCNNRRKKKQDQGNPHEETPM 342

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719540 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Listing list 45 summaries

Database: SWISSPROT_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	772	43.4	339	1 K101_HUMAN	Q15391 homo sapien
2	694	39.0	305	1 K101_HUMAN	Q35881 ratius norv
3	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
4	411.5	23.1	376	1 C9RY_MOUSE	Q97166 mus musculu
5	409.5	22.0	381	1 GPRY_HUMAN	Q99166 mus musculu
6	394	22.2	342	1 PAFR_HUMAN	P21556 camv porce
7	392.5	22.1	342	1 PAFR_HUMAN	P21556 camv porce
8	379.5	21.3	361	1 EH12_HUMAN	Q95003 sus scrofa
9	367	20.6	345	1 CLT2_PIG	Q62035 mus musculu
10	366	20.6	341	1 PAFR_MOUSE	P46002 ratius norv
11	362	20.4	341	1 PAFR_RAT	P32250 gallus gall
12	357.5	20.1	346	1 P2YF_CHICK	Q98755 homo sapien
13	347.5	19.5	346	1 CLT2_HUMAN	P79928 xenopus lae
14	347.5	19.5	537	1 P2Y8_XENLA	Q92041 mus musculu
15	344	19.3	309	1 CLT2_MOUSE	Q92459 ratius norv
16	339.5	19.1	309	1 CLT2_RAT	P25104 bos laurus
17	339	19.1	359	1 AG2R_BOVIN	Q92459 ratius norv
18	338	19.0	344	1 P2Y5_HUMAN	P43657 homo sapien
19	334	18.8	359	1 AG2R_SHEEP	Q77590 ovus ailes
20	329.5	18.5	339	1 GPRH_HUMAN	Q13304 homo sapien
21	329	18.5	359	1 AG2S_HUMAN	Q13725 homo sapien
22	328	18.4	340	1 CLT1_PIG	Q95002 sus scrofa
23	327	18.4	359	1 AG2P_PIG	P30555 sus scrofa
24	325	18.3	359	1 AG2R_CANFA	P43240 canis fami
25	323.5	18.3	359	1 PAR2_MOUSE	P55086 mus musculu
26	321	18.3	359	1 AG2R_KAHIT	P34976 oryctolagus
27	321	18.1	359	1 AG2R_HUMAN	P30556 homo sapien
28	320	18.0	359	1 AG2P_CAVIO	Q94677 homo sapien
29	320	18.0	370	1 P2Y9_HUMAN	Q15743 homo sapien
30	319.5	18.0	365	1 GPR6_HUMAN	P25095 ratius norv
31	319	17.9	359	1 AG2R_RAT	P29089 ratius norv
32	319	17.9	359	1 AG2S_RAT	P29089 ratius norv
33	318	17.9	359	1 AG2R_MOUSE	P29154 mus musculu

34	316.5	17.8	398	1 OPRM_RAT	P33535 ratius norv
35	316	17.8	359	1 AG2S_MOUSE	P29755 mus musculu
36	316	17.8	377	1 AP1_RAT	Q91843 ratius norv
37	316	17.8	397	1 PAR2_RAT	Q63645 ratius norv
38	313.5	17.6	380	1 AP1_HUMAN	P35414 homo sapien
39	313.5	17.6	401	1 OPRM_PIG	Q95247 sus scrofa
40	312	17.5	359	1 AG2R_BOVIN	Q35210 meriones un
41	312	17.5	401	1 OPRM_BOVIN	P79350 bos laurus
42	311	17.5	369	1 PAR3_MOUSE	Q98675 mus musculu
43	310.5	17.5	362	1 AG2R_XENLA	P32303 xenopus lae
44	310.5	17.5	463	1 AG2S_XENLA	P35373 xenopus lae
45	310	17.4	374	1 PAR3_HUMAN	Q00254 homo sapien

ALIGNMENTS

RESULT	ID	STANDARD	PROT	338 AA
K101_HUMAN	K101_HUMAN			
AC	Q15391			
DT	15-JUL-1998 (Ref. 36, Created)			
DT	15-JUL-1998 (Ref. 36, Last sequence update)			
DT	30-MAY-2000 (Ref. 39, Last annotation update)			
DE	Probable G protein-coupled receptor KIAA0001.			
CN	KIAA0001.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain marrow;			
RX	MEDLINE=96051387; PubMed=7584026;			
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawabayashi Y.,			
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;			
RT	"Prediction of the coding sequences of unidentified human genes. I.			
RT	The coding sequences of 40 new genes (KIAA0001-KIAA0040) derived			
RT	analysis of randomly sampled cDNA clones from human immature myeloid			
RT	cell line KG-1."			
RL	DNA Ref. 1:27-35(1994)			
CC	-1- FUNCTION: OPRM1 receptor			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	PROBABLE ORTHOLOG OF RAT VTR 15-20.			
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch).			
CC	or send an email to license@sib.ch).			
DR	EMBL: D13626; BAA02791.1; -			
DR	CCRD: GCR-0594; -			
DR	InterPro: IPR000276; GPCR_Rhodopsin			
DR	PIR: P00001; 76m.1; 1.			
DR	PROSITE: PS00237; G_PROTEIN_PTEP_F1 1; FALSE NEG.			
DR	PROSITE: PS00262; G_PROTEIN_PTEP_F1 2; 1.			
KW	G-protein coupled receptor.			
FT	DOMAIN	1	29	
FT	TRANSMEM	30	55	
FT	DOMAIN	51	55	
FT	TRANSMEM	56	76	
FT	DOMAIN	77	96	
FT	TRANSMEM	97	117	
FT	DOMAIN	118	139	
FT	TRANSMEM	140	160	
FT	DOMAIN	161	188	
FT	TRANSMEM	189	209	
FT	DOMAIN	210	234	
FT	TRANSMEM	235	255	

QY 268 VITLAVFETVYVFFHARIVYLSQTRVDFVTAENLEFYVKESTLWTLSTNAQIDPPT 297
 DB 261 SFVLLIFLFFGVYHAFREIYISQSL NVSSCYWKEIILIKTNIMLVSSNSQLDEVM 319
 QY 298 YFLLAKSPKRSLSLSML 414
 DB 420 YFLMSSNIRKIMQQL 342
 RESULT 5
 GPROT_HUMAN STANDARD: PRI: 481 AA.
 ID GPROT_HUMAN STAN:0953: PRI: 481 AA.
 AC 090953: 095353:
 DT 16 OCT 2001 (Rel: 40, Created)
 DT 16 OCT 2001 (Rel: 40, Last sequence update)
 DT 01 MAR 2002 (Rel: 41, Last annotation update)
 DE Probable G protein coupled receptor GPR34.
 GN GPR34.
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
 NC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo
 NCBI_TaxId=9606;
 OX 1)
 KN SEQUENCE FROM N.A.
 KC TISSUE: testis.
 KC MEDLINE: 99426137; PubMed: 10495919;
 KA Scholte F., Scholz A., Grosse K., Schade R., Heuklein P.,
 KA Scholte F., Guderham T.,
 KA 7A novel subgroup of class I G protein coupled receptors.*;
 KL Biochem. Biophys. Acta 1446:57-70(1999).
 KN 12)
 KN SEQUENCE FROM N.A.
 KC MEDLINE: 99156852; PubMed: 10046181;
 KA Mitchell A., Sawadogo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
 KA Im D., Lynch K.R., George S.R., O'Dowd B.F.,
 KA Discovery of three novel orphan G-protein-coupled receptors.*;
 KL Genomics 56:12-21(1999).
 KN 13)
 KN SEQUENCE FROM N.A.
 KC MEDLINE: 20444921; PubMed: 10982042;
 KA Jacob F.K., Brothammer M., Pesch K., Zrenner E., Berger W.,
 KA Mehlert A., Pesch C.M.,
 KA Physical mapping and exclusion of GPR34 as the causative gene for
 KA congenital stationary night blindness type 1.*;
 KL Hum. Genet. 107:89-91(2000).
 KN 14)
 KN SEQUENCE FROM N.A.
 KC TISSUE: placenta;
 KA Isodat T., Oda T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 KA Nishikawa T., Nagai K., Sugano S., Takahashi Fujii A., Hara H.,
 KA Tanase T., Momura Y., Tohya S., Komai T., Hara R., Takeuchi K.,
 KA Arita M., Nakamura Y., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 KA Wakamatsu A., Nakamura Y., Nagahata K., Masuko Y., Oshima A.,
 KA Nucleic acid sequence project.*;
 DT Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
 DT 1) FUNCTION: ORPHAN RECEPTOR.
 DT 2) SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 DT 3) TISSUE SPECIFICITY: BROADLY EXPRESSED.
 DT 4) SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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 DT or send an email to license@sib-sib.ch).
 DB EMBL: AF036686; MD5:69541.1;
 DB EMBL: AF18670; MD5:7248.1;
 DB EMBL: AK027780; MD5:5462.1;
 DB MM: 600241;
 DB InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_FL_1;
 DR PROSITE: PS0262; G-PROTEIN_RECP_FL_2; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 61
 FT TRANSMEM 62 82
 FT DOMAIN 83 88
 FT TRANSMEM 89 109
 FT TRANSMEM 110 128
 FT TRANSMEM 129 149
 FT TRANSMEM 150 171
 FT TRANSMEM 172 192
 FT TRANSMEM 193 216
 FT TRANSMEM 217 237
 FT TRANSMEM 238 259
 FT TRANSMEM 270 290
 FT TRANSMEM 291 310
 FT TRANSMEM 311 331
 FT TRANSMEM 332 381
 FT DISULFID 127 204
 FT CARBOHYD 28 28
 FT CARBOHYD 36 36
 FT CARBOHYD 42 42
 FT CARBOHYD 200 200
 FT CARBOHYD 295 295
 FT CONFLICT 181 181
 FT CONFLICT 181 181
 SQ SEQUENCE 381 AA; 43860 MW; 491FC0165624379 CNG64;
 Query Match 23.0%; Score 409.5; DH 1; Length 381;
 Host Local Similarity 32.3%; Pred. No. 6,7e 21;
 Matches 102; Conservative 53; Mismatches 152; Indels 9; Gaps 7;
 QY 2 QAVDNITSAPGNLSCTRCYKITGVLPFLVLPVFPVLTITNGLAMPFPIRKSNTI 60
 DB 32 QPONSATP-NVTCPPMDKLSIVLTTSVSVFVGVGLVNIAMVFLGIRKRSIQ 90
 QY 61 IFKNTVSDLMILTFPERKISDAKLGTPRTVCQVSVIEFYTVISISFLGLTI 120
 DB 91 IYLVNVAIDLLIFLPFRIMYHINQNKWTGLGVKVGFLFYVMNYISILGLIST 150
 QY 121 DRYQKTRPRKSNIPKNIJGAKILSVIWAHPPLSLRNMLITNQPDKVKKCSPIKS 180
 DB 151 DRYIKINRSIQKALITKOSIVCCIV-MIALGFLMLITLKKGHSNMGFIYRD 209
 QY 181 EFGLVHMEIVNYICQVIFWVINFIVICVTLTKELR-SYVTR--GVGVPRKRVVK 247
 DB 210 KNAKCAIPLNPLVVMWMLPILILISYIKICKNLIKRSKRSPKPSKAVATARN- 267
 QY 238 VTIIVAVFICVPRFIFARIVYLSQTRVDFCTVNTLFLVKESTLWTLSTNAQIDPPT 297
 DB 261 SFVLLIFLFFGVYHAFREIYISQSL NVSSCYWKEIILIKTNIMLVSSNSQLDEVM 319
 QY 298 YFLLAKSPKRSLSLSML 414
 DB 420 YFLMSSNIRKIMQQL 342
 RESULT 6
 GPROT_HUMAN STANDARD: PRI: 342 AA.
 ID GPROT_HUMAN STAN:0953: PRI: 342 AA.
 AC 090953: 095353:
 DT 01-MAY-1992 (Rel: 22, Created)
 DT 01-MAY-1992 (Rel: 22, Last sequence update)
 DT 16 OCT 2001 (Rel: 40, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).
 GN PAFR OR PAFR.
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
 NC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 NCBI_TaxId=9606;
 OX 1)
 KN SEQUENCE FROM N.A.
 KC TISSUE: platelet;
 KA Isodat T., Oda T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 KA Nishikawa T., Nagai K., Sugano S., Takahashi Fujii A., Hara H.,
 KA Tanase T., Momura Y., Tohya S., Komai T., Hara R., Takeuchi K.,
 KA Arita M., Nakamura Y., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 KA Wakamatsu A., Nakamura Y., Nagahata K., Masuko Y., Oshima A.,
 KA Nucleic acid sequence project.*;
 DT Submitted (MAY 2001) to the EMBL/GenBank/DBJ databases.
 DT 1) FUNCTION: ORPHAN RECEPTOR.
 DT 2) SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 DT 3) TISSUE SPECIFICITY: BROADLY EXPRESSED.
 DT 4) SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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 DT the European Bioinformatics Institute. There are no restrictions on its
 DT use by non-profit institutions as long as its content is in no way
 DT modified and this statement is not removed. Usage by and for commercial
 DT entities requires a license agreement (See <http://www.isb-sib.ch/annotation/>
 DT or send an email to license@sib-sib.ch).
 DB EMBL: AF036686; MD5:69541.1;
 DB EMBL: AF18670; MD5:7248.1;
 DB EMBL: AK027780; MD5:5462.1;
 DB MM: 600241;
 DB InterPro: IPR000276; GPCR_Rhodopsin.

RESULT 10

PAPR_MOUSE

STANDARD: PRT: 341 AA.

15-000-1998 (Rel. 36, Created)

15-000-1998 (Rel. 36, Last sequence update)

15-000-1998 (Rel. 36, Last annotation update)

Platelet activating factor receptor (PAF-R).

PAPR

Mus musculus (Mouse).

Enkayoria: Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI Taxid: 10090;

[1]

SEQUENCE FROM N.A.

MEDLINE: 96259129; PubMed: 8670084;

Mama M., Shimizu T., Nakamura M., Waga I., Kume K., Izumi T.,

*A murine platelet activating factor receptor gene cloning,

chromosomal localization and up-regulation of expression by

lipopolysaccharide in peritoneal resident macrophages.*

Biochem. J. 314:671-676(1996).

FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC

PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-

MUSCLE CONTRACTIONS AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS

ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-

CALCIUM SECOND MESSENGER SYSTEM.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL: U00872; HA09468.1;

GCRD: GCR1618;

MD: M106066; Pfaff-

InterPro: IPR000276; GPCR_Rhodopsn.

Plam: PF00001; 7tm_1; 1.

PRINTS: PR01153; PAFRECEPTOR.

PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;

PROSITE: PS02623; G-PROTEIN_RECEP_F1_2; 1.

G-PROTEIN COUPLED RECEPTOR; Transmembrane; Glycoprotein;

Chemical rxn:

DOMAIN 1 16 EXTRACELLULAR (POTENTIAL);

DOMAIN 17 38 1 (POTENTIAL);

DOMAIN 18 54 CYTOPLASMIC (POTENTIAL);

DOMAIN 19 74 2 (POTENTIAL);

DOMAIN 20 91 EXTRACELLULAR (POTENTIAL);

DOMAIN 21 92 1 (POTENTIAL);

DOMAIN 22 113 CYTOPLASMIC (POTENTIAL);

DOMAIN 23 114 4 (POTENTIAL);

DOMAIN 24 155 EXTRACELLULAR (POTENTIAL);

DOMAIN 25 184 5 (POTENTIAL);

DOMAIN 26 205 CYTOPLASMIC (POTENTIAL);

DOMAIN 27 213 6 (POTENTIAL);

DOMAIN 28 254 6 (POTENTIAL);

DOMAIN 29 275 EXTRACELLULAR (POTENTIAL);

DOMAIN 30 276 7 (POTENTIAL);

DOMAIN 31 341 CYTOPLASMIC (POTENTIAL);

DOMAIN 32 4 4 N-LINKED GLYCAC. (POTENTIAL);

DOMAIN 33 169 N-LINKED GLYCAC. (POTENTIAL);

DOMAIN 34 173 BY SIMILARITY

DOMAIN 35 173 BY SIMILARITY

DOMAIN 36 173 BY SIMILARITY

DOMAIN 37 173 BY SIMILARITY

DOMAIN 38 173 BY SIMILARITY

DOMAIN 39 173 BY SIMILARITY

DOMAIN 40 173 BY SIMILARITY

DOMAIN 41 173 BY SIMILARITY

DOMAIN 42 173 BY SIMILARITY

DOMAIN 43 173 BY SIMILARITY

Best Local Similarity 29.9%; Pred. No. 4,9e-18;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

DB 20 DYKTYLLEPFLVTEFFVGLITNGLAMRIFQI--RSKSNFI-TLTKNTVSDLLMLT 76

DB 10 DSEPRYTLFPIVSVIFHGVANGVAVIWPANLYPSKRIKIKIMVNIIMADLFLI 69

DB 77 PPFPLSDANKGCPHFGCVSVIFPFMYISIFGLITIDYRQKTRPKSNRK 136

DB 70 LPLMIVYYNEDGMLIFLFLCNVAGCLEPFIINTCSVAFELVITNRYQAVYIKTKAQAT 129

DB 137 NLGAKILSVIWMF-----PILSLPNNMILINRQPKNVKKCSPLKSPG---LVMPH 188

DB 130 TRKGISLILVSIWVATVATAPLATDSTNLYPNKDSQNIIRCFHRYPPSVIIVAVH 189

DB 189 IVNYICQVIFMINFLI-VIACYLLIKELRSVRTGVSKVKKVKNVVFIIIVFFI 247

DB 190 FIACPFLVPLIIFYCNVILHILITDPMKQO--KAGV---KRAIMWCTVIAVPI 243

DB 248 CVPFHRARIPYTLISQTRDVEPDTAENILFYVKESTILMISLACADLPYFFI/CKSPN 307

DB 244 CFVPHVHVGPLMTLAEIG--YGFNFQAINDAHQITLITLSTNVLDPVLYTFLIKKKR 301

DB 308 -----SLISMICKPNSATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DB 302 HLSKPYMSRMSRKC-SKATS 321

DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor, Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 16
 FT TRANSSEM 17 38
 FT TRANSSEM 39 54
 FT TRANSSEM 55 74
 FT TRANSSEM 75 91
 FT TRANSSEM 92 113
 FT TRANSSEM 114 133
 FT TRANSSEM 134 155
 FT TRANSSEM 156 184
 FT TRANSSEM 185 205
 FT TRANSSEM 206 233
 FT TRANSSEM 234 254
 FT TRANSSEM 255 275
 FT TRANSSEM 276 295
 FT TRANSSEM 341
 FT CARBOHYD 4
 FT CARBOHYD 159
 FT DISULFID 90
 FT SEQUENCE 341 AA; 30204 MW; 104672700-104658-104664;

Query Match 20:48; Score 362; DB 1; Length 341.
 Best local similarity 28.98; Pred. No. 9; 10-18;
 Matches 96; conservative 66; Mismatches 120; Indels 50; Gaps 10;

QY 20 DYKLTQVLPFLTYLFEVGLTNGLAMRIF--FQIRSKNFIELKNVISLMLILF 76
 DB 10 DSEPRYLPLVSVILVGVANGVYAWFALYPSKKINEIKIHVNITVALILMLI 69
 QY 77 FPEKILSDAKLGTPLRFVQVTSVFETVYISFELITIDPQKTRPFKTSNPK 136
 DB 70 LPLMTVYVSEGDIVKELCNLAGLEFINTYCSVAFLVITVNRQVAVPIKTAQT 129
 QY 137 NLGAKILSVYNAFM-----PLISLPNMHITNRPDKVKKC-----S 176
 DB 130 TRRGITLSLVWISIAATSYFLADSTNVVPRKDSGNITKCFEHYEPYSPVILVHI 189
 QY 177 ELKSEFSLVMEIYNYICQVIFNPLIVICYTLTKELRYSVPTPSVSKYPRKVVN 236
 DB 190 FIIISCFPIYF-----LIFCNMVI---HLLIFRP-----VRQKRPYKRRALIM 234
 QY 237 KVTIIAVFICEVPEHPIPIYTLISQTRDFVDCIAENTLFYKESTLWTSINACIDPF 296
 DB 234 -VTVLAVFVFEVHHVQVLPMTLDELG--YQTFHQAINIHAQITLVLSIN-VILFV 250
 QY 297 IYFPLCKSPK-----SLISMALCYNSAIS 321
 DB 291 IYFPLCKSPK-----SLISMALCYNSAIS 321

RESULT 12
 P2Y5_CHICK STANDARD; PRT: 308 AA.
 ID P2Y5_CHICK
 AC P32250;
 DT 01-OCT-1993 (Ref. 27, Created)
 DT 01-OCT-1993 (Ref. 27, Last sequence update)
 DT 15-JUL-1998 (Ref. 36, Last annotation update)
 DE P2Y purinoceptor 5 (P2Y5) (purinergic receptor 5) (6n1).
 GN P2Y5.
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN 11
 RP SEQUENCE FROM N A
 RC TISSUE=T-cell;
 RX MEDLINE=93329056; PubMed=8393036;
 RA Kaplan M.H., Smith D.L., Sundick R.S.;
 RT Identification of a G protein coupled receptor induced in activated

RT T cells.";
 FL J. Immunol. 151:628-636(1993).
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC 1- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
 CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL: 104109; AM006587.1;
 DB HSSP: P34966; 1DDO
 DB GPCRdb: GPCR_0689;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01067; P2Y5PRNOCPT.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor, Transmembrane; Glycoprotein; Lipoprotein;
 FT DOMAIN 1 16
 FT TRANSSEM 17 43
 FT TRANSSEM 44 52
 FT TRANSSEM 53 76
 FT TRANSSEM 77 89
 FT TRANSSEM 90 109
 FT TRANSSEM 110 130
 FT TRANSSEM 131 151
 FT TRANSSEM 152 178
 FT TRANSSEM 179 206
 FT TRANSSEM 207 224
 FT TRANSSEM 225 250
 FT TRANSSEM 251 269
 FT TRANSSEM 270 289
 FT TRANSSEM 290 308
 FT CARBOHYD 5
 FT CARBOHYD 281
 FT DISULFID 86
 FT SEQUENCE 308 AA; 35597 MW; 4214596963386F7D CRC64;

Query Match 20:18; Score 357; DB 1; Length 308;
 Best local similarity 29.58; Pred. No. 1; 70-17;
 Matches 87; conservative 68; Mismatches 125; Indels 15; Gaps 8;

QY 14 TSLCTDQVYITQVLPFLTYLFEVGLTNGLAMRIF--FQIRSKNFIELKNVISLMLILF 72
 DB 3 SSNCSTEDSEFKTYLGVCSNMFVGLIANGVAIYFTFLTKVRNRTTYMLNLSIDL 62
 QY 73 MLTPPEKILSDAKLGTPLRFVQVTSVFETVYISFELITIDPQKTRPFKTSNPK 132
 DB 63 FVTLPPEKILYEV-VNRPFGVGLKISTVLTETNMYSGLSLTLCISVRELAIVHPRS 121
 QY 133 SNRKNLGAKILSVYNAFMFLSLPNNLT--TNQPPDKVKKC--SELKSEFSLVMEI 188
 DB 122 KILKTKRKAHIVCAVAVITVLAWSIYASHFQSIHQ--NNIHQKICHEN--PSIMVILSR 180
 QY 189 IVNYITQVIFNPLIVICYTLTKELRYSVPTPSVSKYPRKVVNVPVITIAVFFIC 248
 DB 181 IYFIIIVSEFIPILINVTSTIMVLPFLKKPLTLR NKLKKRVAKMIVHLEVIFPC 248
 QY 249 FVPEHPIPIYTLISQTRDFVDC--TAENTLRYVKSTSLMLISINACIDPFYFP 300
 DB 239 FVYNTITLILYSLMTQTWININSVVITAVTMYF---TQVAVSN--CPPIYYTF 290

RESULT 13
 CLF2_HUMAN

[illegible]

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia, Pipoidae, Pipidae;
 CC Xenopodidae; Xenopus;
 CC NCBI_TaxID=8335;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Neural plate;
 RX MEDLINE:97284734; PubMed:9139711;
 RA Jordanov V D., Dale I., King H.F., Whitlock N., Hornstock G.;
 RT "Early expression of a novel nucleotide receptor in the neural plate
 of Xenopus embryos";
 PL J. Biol. Chem. 272:12583-12590(1997).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, GTP, CTP AND UTP.
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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 CC -----
 DR EMBL: X99563; CAA68213.1;
 DR HSSP: P34966; 1DDP.
 DR GCRDB: GCR_1419;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; G_PROTEIN_RECPT_P1_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_P1_2; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
 KM G-protein coupled receptor: Transmembrane; Glycoprotein
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 50 70 1 (POTENTIAL)
 FT DOMAIN 71 79 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 80 100 2 (POTENTIAL)
 FT DOMAIN 101 118 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 119 139 3 (POTENTIAL)
 FT DOMAIN 140 161 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 162 182 4 (POTENTIAL)
 FT DOMAIN 183 210 5 (POTENTIAL)
 FT TRANSMEM 211 231 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 232 254 6 (POTENTIAL)
 FT TRANSMEM 255 275 7 (POTENTIAL)
 FT TRANSMEM 276 292 7 (POTENTIAL)
 FT TRANSMEM 293 316 7 (POTENTIAL)
 FT DOMAIN 317 517 CYTOSOLASMIC (POTENTIAL)
 FT DOMAIN 518 537 CYTOSOLASMIC (POTENTIAL)
 FT CARBOHYD 116 193 N-LINKED (GLCNAC...) (POTENTIAL)
 FT CARBOHYD 26 26 N-LINKED (GLCNAC...) (POTENTIAL)
 FT SEQUENCE 537 AA: 62024 MW: 10274612 Da; pI=4.2; pKa=6.4.
 Query Match 19.58; Score 347.5; DR 1; Length 537;
 Best local Similarity 29.38; Prod No 1 3e-16;
 Matches 943; Conservative 60; Mismatches 157; Indels 7; Gaps 5.

QY 180 SEFVLWHEIVNLCGVLEWLNFLVGVPLITKELSPVPTGVSQVPRKRVNK 247
 DB 199 PDPRARYVSTALMCLGIPICLLIADCVGLMRELMKPLVSGNOOLISYKRSIKTI 258
 QY 238 VELLIAVPEICVPPHARIPYLLISQTRVDYDCAENILVYKRSILMLISLACDIPFI 247
 DB 249 IFVMAI-FAIFPMPEHITPTIYYVAPLIGI KYALVNIYTVYVTPPLSANSQDPIIL 416
 QY 298 YFPIICKSPRNSLSIMK 314
 DB 317 YELANDRYRRRIKTRV 333
 RESULT 15
 ID CLF2_MOUSE STANDARD; PRT; 309 AA.
 AC 0920AT;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Cysteinyl leukotriene receptor 2 (CysLT2).
 GN CysLT2 OR CysLT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Mus.
 CC NCBI_TaxID=10090;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX PubMed:11591709;
 RA Bai Y., Yang G., Galyczenki H., Figueroa D.J., Austin G.P.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk G.D.;
 RT "The murine cysteinyl leukotriene 2 (CysLT2) receptor, cDNA and
 RT genomic cloning, alternative splicing, and in vitro
 RT characterization";
 PL J. Biol. Chem. 276:47480-47495(2001).
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol
 CC calcium second messenger system. The rank order of affinities for
 CC the leukotrienes is LTC4 > LTD4 > LTE4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
 CC expression in the spleen, thymus and adrenal gland, and lower in
 CC the kidney, brain and peripheral blood leukocytes.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb.ch).
 CC -----
 DR EMBL: AF31658; AK97354.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_P1_1; FALSE_NEG.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_P1_2; 1.
 KM G-protein coupled receptor: Transmembrane; Glycoprotein
 FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 27 47 1 (POTENTIAL)
 FT DOMAIN 48 56 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 57 77 2 (POTENTIAL)
 FT DOMAIN 78 98 3 (POTENTIAL)
 FT TRANSMEM 99 119 3 (POTENTIAL)
 FT DOMAIN 120 138 CYTOSOLASMIC (POTENTIAL)
 FT TRANSMEM 139 159 4 (POTENTIAL)
 FT DOMAIN 160 187 5 (POTENTIAL)
 FT TRANSMEM 188 208 5 (POTENTIAL)
 FT DOMAIN 209 229 6 (POTENTIAL)
 FT TRANSMEM 230 250 6 (POTENTIAL)
 FT DOMAIN 251 271 EXTRACELLULAR (POTENTIAL).

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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:42:12 : Search time 13.1 Seconds

(without alignments)
637,676 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MOAVDNILTSAPNHSICTRP

Sequence: 342 SQNPKKFGGCGNPFPPW

Scoring table:

BLOSUM62
Gapop 10.0 : Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA*

1: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*
2: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*
3: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*
4: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*
5: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*
6: /seq2_5/Prodata/42/1aa/5A_TOMR pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	US-08-852-824-2	Sequence 2, Appli
2	823	46.3	333	US-09-221-456-2	Sequence 2, Appli
3	823	46.3	333	US-09-558-740-2	Sequence 2, Appli
4	797	44.8	333	US-08-812-871-1	Sequence 1, Appli
5	772	43.4	325	US-08-467-948A-29	Sequence 29, Appli
6	772	43.4	325	US-08-467-947A-29	Sequence 29, Appli
7	772	43.4	338	US-08-988-876-8	Sequence 8, Appli
8	772	43.4	338	US-09-303-524A-2	Sequence 2, Appli
9	679.5	38.2	358	US-08-988-876-3	Sequence 3, Appli
10	546.5	30.7	293	US-08-467-948A-6	Sequence 6, Appli
11	546.5	30.7	293	US-08-467-947A-6	Sequence 6, Appli
12	488	27.4	319	US-08-702-344-28	Sequence 28, Appli
13	410.5	23.1	326	US-08-118-270-39	Sequence 39, Appli
14	410.5	23.1	326	PCT-US93-08528-39	Sequence 39, Appli
15	392.5	22.1	342	US-08-988-876-9	Sequence 9, Appli
16	379.5	21.3	361	US-08-383-750-4	Sequence 4, Appli
17	379.5	21.3	361	US-08-452-678-4	Sequence 4, Appli
18	379.5	21.3	361	PCT-US93-09636-4	Sequence 4, Appli
19	376	21.2	348	US-08-852-824-17	Sequence 17, Appli
20	374.5	21.1	381	US-08-467-125-2	Sequence 2, Appli
21	374.5	21.1	381	US-08-911-320A-2	Sequence 2, Appli
22	374.5	21.1	381	US-09-217-101-2	Sequence 2, Appli
23	349.5	19.7	302	US-08-467-948A-30	Sequence 30, Appli
24	349.5	19.7	302	US-08-467-947A-30	Sequence 30, Appli
25	339	19.1	344	US-08-467-948A-8	Sequence 8, Appli
26	339	19.1	344	US-08-467-947A-8	Sequence 8, Appli
27	337	19.0	468	US-08-907-223-327	Sequence 327, App

28	329.5	18.5	339	1	US-08-153-848-44	Sequence 44, Appli
29	329.5	18.5	339	2	US-08-812-871-3	Sequence 3, Appli
30	329.5	18.5	339	3	US-09-239-843A-44	Sequence 44, Appli
31	329.5	18.5	339	4	US-09-088-337B-44	Sequence 44, Appli
32	329.5	18.5	339	5	PCT-US93-11153-44	Sequence 44, Appli
33	329.5	18.5	339	6	PCT-US95-07180-2	Sequence 2, Appli
34	329	18.5	359	1	US-08-041-219A-6	Sequence 6, Appli
35	329	18.5	359	2	US-08-417-122-6	Sequence 6, Appli
36	327.5	18.4	395	1	US-08-097-938-2	Sequence 2, Appli
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38	327.5	18.4	395	1	US-08-472-840-2	Sequence 2, Appli
39	327.5	18.4	395	2	US-08-476-976-2	Sequence 2, Appli
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41	325.5	18.3	395	4	US-08-486-673B-2	Sequence 2, Appli
42	325.5	18.3	395	4	US-08-486-673B-5	Sequence 5, Appli
43	325.5	18.3	399	1	US-08-476-000-61	Sequence 61, Appli
44	325.5	18.3	399	1	US-08-472-840-61	Sequence 61, Appli
45	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appli

ALIGNMENTS

RESULT 1
US-08-852-824-2
Sequence 2, Application US/0885282A/C
Patient No. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-protein Coupled Receptors
FILE REFERENCE: 1488,1220000
CURRENT APPLICATION NUMBER: US/09/452-824C
CURRENT FILING DATE: 1997-05-04
NUMBER OF SEQ. ID NOS.: 18
SOFTWARE: Blastp in Ver. 2.0
SEQ ID NO: 2
LENGTH: 342
TYPE: PRT
ORGANISM: genomic
US-08-852-824-2

Query Match	100.0%	Score 1778:	DB 3:	Length 342:
Best local Similarity	100.0%	Pred. No. 1,36-144:		
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1 Sequence 2, Application US/09221456
2 Patent No. 616,899
3 GENERAL INFORMATION:
4 APPLICANT: SATHI, GANESH
5 APPLICANT: HATHI, WENDY
6 APPLICANT: MUIR, ALISON
7 APPLICANT: CHAMBERS, JON
8 APPLICANT: SEZERES, PHILIP
9 TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
10 TITLE OF INVENTION: AND ANTAGONISTS OF THE HINAA81 RECEPTOR
11 NUMBER OF SEQUENCES: 2
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Rainer & Prestia
14 STREET P.O. Box 980
15 CITY: Valley Forge
16 STATE: PA
17 COUNTRY: USA
18 ZIP: 19482
19 COMPUTER READABLE FORM:
20 METHOD TYPE: Diskette
21 COMPUTER: IBM Compatible
22 OPERATING SYSTEM: DOS
23 SOFTWARE: FASTSEQ for Windows Version 2.0
24 CURRENT APPLICATION DATA:
25 FILING DATE: 28 DEC 1998
26 CLASSIFICATION:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 08/956,975
29 FILING DATE: 24 OCT 1997
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Prestia, Paul F
32 REGISTRATION NUMBER: 23,031
33 REFERENCE/BOOKET NUMBER: CH-70318-1
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 610-407-0700
36 TELEFAX: 610-407-0700
37 TELE: 616169
38 INFORMATION FOR SEQ ID NO: 2:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 333 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MULTIPLE TYPE: protein
45 US-09-221456-2
46
47 Query Match 46.3%, Score 823, DB 4, Length 333,
48 Best Local Similarity 48.7%, Pred. No. 4, 6e-63,
49 Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
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51 17 CTDRDKYITGVFLPYLVFVGLTNGLAIRIPFOIRKSNPTPLAKNTVSDILMLIT 76
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66 417 NSATSLSDNNKKKOD 332

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1 Db 313 KRTTASSQENHSSQTD 328
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3 RESULT 3
4 US-09-558-740-2
5 Sequence 2, Application US/09558740
6 Patent No. 6358695
7 GENERAL INFORMATION:
8 APPLICANT: SATHI, GANESH
9 APPLICANT: HATHI, WENDY
10 APPLICANT: MUIR, ALISON
11 APPLICANT: CHAMBERS, JON
12 APPLICANT: SEZERES, PHILIP
13 TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
14 TITLE OF INVENTION: ANTAGONISTS OF THE HINAA81 RECEPTOR
15 FILE REFERENCE: CH-70318-2
16 CURRENT APPLICATION NUMBER: US/09/558,740
17 CURRENT FILING DATE: 2000-04-26
18 PRIOR APPLICATION NUMBER: 08/956,975
19 PRIOR FILING DATE: 1997-10-23
20 PRIOR APPLICATION NUMBER: 09/221,456
21 PRIOR FILING DATE: 1998-12-28
22 SOFTWARE: FASTSEQ for Windows Version 3.0
23 NUMBER OF SEQ ID NOS: 2
24 SEQ ID NO 2
25 LENGTH: 333
26 TYPE: PRT
27 ORGANISM: HOMO SAPIENS
28 US-09-558-740-2
29
30 Query Match 46.3%, Score 823, DB 4, Length 333,
31 Best Local Similarity 48.7%, Pred. No. 4, 6e-63,
32 Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;
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34 17 CTDRDKYITGVFLPYLVFVGLTNGLAIRIPFOIRKSNPTPLAKNTVSDILMLIT 76
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46 317 NSATSLSDNNKKKOD 332
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48 Db 313 KRTTASSQENHSSQTD 328
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50 RESULT 4
51 US-08-812-871-1
52 Sequence 1, Application US/08812871
53 Patent No. 5955303
54 GENERAL INFORMATION:
55 APPLICANT: Au-Young, Janice
56 APPLICANT: Guegler, Karl
57 APPLICANT: Mocong, Cheng
58 TITLE OF INVENTION: NOVEL HUMAN CHRMOKINE RECEPTOR-LIKE
59 TITLE OF INVENTION: PROTEIN
60 NUMBER OF SEQUENCES: 3
61 CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MIM3D101
CLONE: 568897
US-08-812 871 1

Query Match 44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Prod. No. 7.7e-61;
Matches 151, Conservative 57, Mismatches 106, Indels 2, Gaps 1;

QY 17 CREFKRTGVLPFLYVTFVFGVLTNGLAMIFVQISKSNFIFLANTVSDMLLT 76
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DB 75 LPEKILISDHLAPQDLRAVFCVSVIFETMYGVILGLIAPDRFLKIIFPLNITLK 134
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DB 255 VYTHSQTNKKTCDKQNLFLAKETITFLAINTICMPLISIFLCKKTEKTLPCMO--G 312
QY 317 NSATSLSDNKKEDD 312
DB 313 RKTASSQENHSSQTD 328

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RESULT 5
US-08-467-948A-29

Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG

```

APPLICANT: LI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: HUIF, CAROL J.
APPLICANT: SUTTON TII, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/24079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488 1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO. 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Prod. No. 1e-58;
Matches 149, Conservative 60, Mismatches 105, Indels 0, Gaps 0;

QY 6 NLTSAPNTSTCTPDYKRTQVIFPLAYTVLFGVLTNGLAMPFQIPKSNFIFLN 65
DB 2 NSISIQPDSCSONLLITCOIIVLYCMVFACILNCGVSGWIFPVPSKSPITVLMN 61
QY 66 TVISDMLILFPPKILISDAKIGTGPRTFCVTSVIFPYIMYISLPGIILDKYOK 125
DB 62 IVLIDFVMSLTFPRKILISDSGLGFWLNVCEVSAVLFVNMVVSIVFGLISFDYR 121
QY 126 TTRPKTSNPKNLGAKILSVIWMFELISLDPNMLITNROPDRKNVKKCSFLKSEFGV 185
DB 122 IVKPLMISFISQSVSKSLSVIWMMLGLAVNMLITNSVSKVIVYKIELKSLGK 181
QY 186 WHEIVNTICQVTFWIFNLVIVVYTLITKLTYSYVPTFRVGVKVPKKVNVKVFITIAVF 245
DB 182 WKKASNYIFVAIFWIFVLLILVFTATITRKIFKSHLSSFNSTSVKSSRNIFSIIVFV 241
QY 246 FICVPPHAPAKIVYLSQKRVPLDCTAENLIFVYKSESLMISLACIDPFIYFLCKSP 305
DB 242 FVCFVPHIARIPTKQTEAHNSQSKELIRYKETTLLISANVGLDPIITFFLCQPF 301
QY 306 NNSLISMLKCPNSA 319
DB 302 REILCKKIHLPLKA 315

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QY 186 WHFIVNYICGVILWVNFILVIVCYTLITKELYSRVYRTGCVCKVPRKKVNVVFIILAVF 245
 DB 183 MHKASVITVAIFWIVFLLIIVFYTAITTKRKSHLKSSRNSTSYKKSSRNIFSIIVFV 242
 QY 246 FICFVPHFARIPYTLISQTRDVFCTAENTLFEVKESTLMTLSLNAQIDPFIVFELCKSF 305
 DB 243 FVCFVYHIAIRIPYTKSQTFAHVSQSKRLRYMKRFTLLLSAANVCIDPIIVFPLCGVF 302
 QY 306 RNSLISMLKCPNSA 319
 DB 303 RELCKKHLHPLKA 316

RESULT 8
 US-09-303-524A-2
 ? Sequence 2, Application US/0930352AA
 ? Patent No. 6218873
 ? GENERAL INFORMATION:
 ? APPLICANT: CHAMBERS, JONATHAN K.
 ? APPLICANT: STEWART, BRIAN R.
 ? APPLICANT: AMES, ROBERT S.
 ? APPLICANT: SAKAO, HENRI M.
 ? APPLICANT: FOLEY, JIM
 ? APPLICANT: ARNOLD, ANNE ROMANIC
 ? TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
 ? TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
 ? TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
 ? FILER REFERENCE: G950007
 ? CURRENT APPLICATION NUMBER: US/09/303,524A
 ? CURRENT FILING DATE: 1999-04-30
 ? PRIOR APPLICATION NUMBER: 60/083,957
 ? PRIOR FILING DATE: 1998-05-01
 ? NUMBER OF SEQ ID NOS: 2
 ? SOFTWARE: FASTSEQ for Windows Version 3.0
 ? SEQ ID NO 2
 ? LENGTH: 338
 ? TYPE: FRT
 ? ORGANISM: Homo sapiens
 ? US-09-303-524A-2

Query Match 43.4%; Score 772; DB 4; Length 338,
 Best Local Similarity 47.5%; Pred. No. 1,le-58;
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAQNTSLCTRDYKLTGVILPPLIATVILFVGLITNGLAMRIIPQIRKSNMFIILKLN 65
 DB 3 NSTSTQPHBSQSNLITLQOIIIVLYCWFVLAGIILNGVSGMIFHYVVSXKSFIIYLKN 62
 QY 66 TVISDLMLITPEFKILSDAKLITPPLRTFVQVNTSVIYFTMYISISPLGLITIDRYOK 125
 DB 63 IVIADVMSITPEFKILSGSGQWQJLVFVCSAVLFFVNMVYSIVFPGILISDRYRK 122
 QY 126 TTRPFTSNRKNLCAKILSVIWAAPHLISLPMMLITNRQPRKNVKKCSPLKSEFGLV 185
 DB 123 IYKPLTSELOSYSKSLSVIWMMLLELAVPNIITLTMSVFEVYQIGTIELKSELGPR 182
 QY 186 WHFIVNYICGVILWVNFILVIVCYTLITKELYSRVYRTGCVCKVPRKKVNVVFIILAVF 245
 DB 183 MHKASVITVAIFWIVFLLIIVFYTAITTKRKSHLKSSRNSTSYKKSSRNIFSIIVFV 242
 QY 246 FICFVPHFARIPYTLISQTRDVFCTAENTLFEVKESTLMTLSLNAQIDPFIVFELCKSF 305
 DB 243 FVCFVYHIAIRIPYTKSQTFAHVSQSKRLRYMKRFTLLLSAANVCIDPIIVFPLCGVF 302
 QY 306 RNSLISMLKCPNSA 319
 DB 303 RELCKKHLHPLKA 316

RESULT 9

US-08-988-876-3
 ? Sequence 3, Application US/08988876
 ? Patent No. 6063596
 ? GENERAL INFORMATION:
 ? APPLICANT: Lal, Preeti
 ? APPLICANT: Bandman, Olga
 ? APPLICANT: Hillman, Jennifer L.
 ? APPLICANT: Yoo, Henry
 ? TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 ? TITLE OF INVENTION: WITH IMMUNE RESPONSE
 ? NUMBER OF SEQUENCES: 9
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: Incyte Pharmaceuticals, Inc.
 ? STREET: 3174 Porter Drive
 ? CITY: Palo Alto
 ? STATE: CA
 ? COUNTRY: USA
 ? ZIP: 94304
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/988,876
 ? FILING DATE: Herewith
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Billings, Lucy J.
 ? REGISTRATION NUMBER: 36,749
 ? REFERENCE/DOCKET NUMBER: PR-0441 US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 650-855-0555
 ? TELEFAX: 650-845-4166
 ? TELEX:
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 358 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? IMMEDIATE SOURCE:
 ? LIBRARY: PROSTUT09
 ? CLONE: 1650519
 ? US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 358;
 Best Local Similarity 43.7%; Pred. No. 9e-51;
 Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

QY 6 NLTSAQNTSLCTRDYKLTGVILPPLIATVILFVGLITNGLAMRIIPQIRKSNMFIILKLN 64
 DB 25 NNSDGRKGNNTL---HNEFDIVLIVFLVILIFVASILNLGLAVVIFHHIRKTSFIYIK 81
 QY 65 NTVISDLMLITPEFKILSDAKLITGPLRTFVGVNTSVIYFTMYISISPLGLITIDRYOK 124
 DB 82 NIVVADMLITLTPFRIVHDAGFGWYRKFIIDKRTSVLFTYANNYSIVPLGLISIDRYL 141
 QY 125 KTRPFTSNRKNLCAKILSVIWAAPHLISLPMMLITNRQPRKNVKKCSPLKSEFGLV 184
 DB 142 KVVKFEQDSRMYSITFTKVLSCVWVIVAVLSLEPNIILTNQPTEDNIDHSKLSPLGV 201
 QY 186 WHFIVNYICGVILWVNFILVIVCYTLITKELYSRVYRTGCVCKVPRKKVNVVFIILAVF 243
 DB 202 KMTAVTVNSCLFVAVLVILIGCTIAISRTHRS--SRQFTSQSSRRKRNOSTIRVVA 259
 QY 244 VFIQVPHFARIPYTLISQTRDVFCTAENTLFEVKESTLMTLSLNAQIDPFIVFELCKSF 303
 DB 260 VFTQCFILPYHICRMDSITPSHLDRIIDBSAQKILVYCKKFTLITLACNVCIADPIIVFPMCK 319

QY 404 SE 405
14
DB 420 SE 421

RESULT 10

US-08-467-948A-6
Sequence 6, Application US/08467948A
Patent No. 6090164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CHU, LIANG
APPLICANT: NI, JIAN
APPLICANT: CHEN, ZHEN
APPLICANT: BULL, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06 JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 06 MAR 1995
ATTORNEY/AGENT INFORMATION:
NAME: STEEPE, ERIC K.
REGISTRATION NUMBER: 46,688
REFERENCE/DOCKET NUMBER: 1488, 1:46023/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-948A-6

Query Match 40.7%; Score 546.5; DB 2; Length 293;
Best Local Similarity 42.3%; Pred. No. 17e-39;
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;

QY 17 CTDRYKLTQVLFLLTYLFEVGLITNGLAMRIFQIRKSNFIIFLKNTVISDLIMLT 76
15 CKDRIRIVQVLPALTYVVLITGLINTALWVHIPISSSTFIYIKNTIVADILMTLM 74
QY 77 FPKKLSIAKLTGTPLFVQVTSVFPTMYISIFGLITIDRYOKTRPKTSNPK 136
75 LFKKLSIAKLTGTPLFVQVTSVFPTMYISIFGLITIDRYOKTRPKTSNPK 134
QY 137 NLGAKLSVAVIWMFPLSLPNMILINRQIRKNNKCSPLKSPGIVWHEIVNYICGV 196
135 KPWKKTIVSIFIPWFPIISLNMILSNKRPATISSVKKCSLKGPIGLKWHQVNNICGF 194
QY 137 IIVNLTIVIVYTLITKE LYSVYVTPGVKVPKKVNVVEIIVAFVIFGVF- 251

DB 195 IFWTFIILMLVEYVVIARKYMLIESPVRTETKSKAKYLLSWLSLVLHFIISPE 254
QY 252 RHPARIPTLSOTRQVFDYAFNTLPVYKKESTLW 285
DB 255 FHLTVKPTIRLT---VDKTI-NCLLEKRLQSLFW 284

RESULT 11

US-08-467-947A-6
Sequence 6, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: CHEN, ZHEN
APPLICANT: BULL, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06 JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEEPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 1140002/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-947A-6

Query Match 30.7%; Score 546.5; DB 3; Length 293;
Best Local Similarity 42.3%; Pred. No. 17e-39;
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;

QY 17 CTDRYKLTQVLFLLTYLFEVGLITNGLAMRIFQIRKSNFIIFLKNTVISDLIMLT 76
15 CKDRIRIVQVLPALTYVVLITGLINTALWVHIPISSSTFIYIKNTIVADILMTLM 74
QY 77 FPKKLSIAKLTGTPLFVQVTSVFPTMYISIFGLITIDRYOKTRPKTSNPK 146
75 LFKKLSIAKLTGTPLFVQVTSVFPTMYISIFGLITIDRYOKTRPKTSNPK 144
QY 137 NLGAKLSVAVIWMFPLSLPNMILINRQIRKNNKCSPLKSPGIVWHEIVNYICGV 196
135 KPWKKTIVSIFIPWFPIISLNMILSNKRPATISSVKKCSLKGPIGLKWHQVNNICGF 194

QY 197 FMINPLIVVCTLLPKR-----LVHSVVRTRGVKVPKRVNKKVPIIIIAVFICPPV- 251
DB 195 IMVIVLILVIVVIAKKMILIESPKRVTEKTEKSMWAKYLLSLMSICVLHFIISPE 254
QY 252 PRRARIPVTLISQTRVDFCTAENTLFFVKESTLW 285
DB 255 FMHIVVPTIKRLT---VDCR-NCCLLKKKLSFW 284

RESULT 12

US-08-702-344-28

Sequence 28, Application US/08702344

Patent No. 5723415

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Lavallee, Edward

APPLICANT: Racto, Lisa

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SELECTED PROTEINS AND POLYPEPTIDES

TITLE OF INVENTION: ENCODING THEM

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-702-344

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 319 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-344-28

Query Match 27.4%; Score 488; DB 1; Length 319;

Best Local Similarity 34.5%; Pred. No. 1.8e-34;

Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 MNSICTRIYKILTOVLPPLIVLFFVGLITNGLAMRIFFQIRSKSNFI-IFLKNVVISDL 71
DB 3 NSSFFCIPYKIDLP-FTTFYFLVFLVGLISCFATMAEIKNTNRCVSTILMLLADF 61
QY 72 IMITLTPKILISDAKIGTP--LRTFVGVVSVIIFPTMYISISLGLITIDRYQKTRP 129
DB 62 ILITLAPKIVVD--IGVAPWKIKLIFHCQVIACTIYINMYISILFLAFVSDRCIQITHS 119
QY 130 FRTSPKMLKAKILISVYIMAFMELISLNNILTRQPKDKNVKCKSLKSEFGLVMEI 189
DB 120 KTVIYIOPGCAKMIISVWMLVAILIVPNNMIPKIDIKESNVCCMIFKKEFGKNNHLL 179

QY 190 VNYICOVIFMINF-LIVIVCTLLITKELYSVVRTRGVKVPKRVNKKVPIIIIAVF 247
DB 180 TNFICVAF-LNFSAILIISNGLVIRQIRN-----KQENPNPKKLLINLLVTTGYII 234
QY 248 GEPFHFARIPVTLISQTRVDFCTAENTLFFVKESTLWLSLACDPFIYFLKCSFN 307
DB 235 GFVPHIVIRIYPTLSQFVETIDCSIRISLFFKAKKATILLAVSNICPPHIIYHISKAFRS 294
QY 308 SLI-----SMLKCPNSA 319
DB 295 KVFETASPKEKTKAKKEKLCENNA 319

RESULT 13

US-08-118-270-39

Sequence 39, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

TITLE OF INVENTION: PREPEPTIDS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-118-270

FILING DATE: 09-SEP-1993

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MIPPIY-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 326 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-118-270-39

Query Match 23.1%; Score 410.5; DB 1; Length 326;

Best Local Similarity 32.2%; Pred. No. 7.7e-28;

Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

QY 27 LPELIVLFFVGLITNGLAMRIFFQIRSKSNFI-IFLKNVVISDLMLTFFPKILSD 84
DB 1 LPIIVISILIVIGLIANGVYIAVFAHRYPSKKMFIKIFVNLIVADILFLITLPIWIVY 60
QY 85 AKIGTGLPFFVGVVSVIIFPTMYISISLGLITIDRYQKTRPKTSNPKMLDCAKIL 144
DB 61 SNGSNMFLFELNGLAGCEFFINYSVALGLVITTFQAVKYPFIKTQVATTKRGIAL 120
QY 145 SVVITW-----AFMFLISLNNILTRQPKDKNVKCKSLKSEFGLVMEI 194

10 121 NIVAVVAIVAASVETIYVMDISIVVSNAGSNTTRC-PEYERKSGKSVLIIH-----IC 174

07 195 CVI FMNFIIVIVYTIITFEIYPSVYVTVGKVPYKPVNVVFIIVIAVEFTYVPVPI 26

06 175 IVDSIVFVEILLIETPVIITHTLEGPYKQVNAEV-PPALMVGVVIVIAVEFVPIIH 233

07 254 FAKIVYHSIDRVIDFAENILEYVKSTHMLSTINACIDPFIYFELCKSPKSLISML 313

06 214 KQVLIWLTAEI-CHMPSNSHDAINADVTLTLESTVGLDPSVLYCTLTFERKHLSKEL 292

07 814 KQVNSATISQINPKPKFVETGTPMEFTPM 442

06 293 NIMPSNKGSPVIRIOTIEMALPFINHTV 421

REF: 14

1. GENERAL INFORMATION:
Sequence 49, Application PC/US9308528
Ref US93 08528 49

APPLICANT: NEW YORK UNIVERSITY
TITLE OF INVENTION: POLYPEPTIDES OF G-COILED PROTEIN
TITLE OF INVENTION: REPEATERS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 448
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 SOUTHB STREET, N.W., SUITE 300
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPILED BY: FOR COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PATENT IN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US73/08528
FILING DATE: 09 SEP 1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10 SEP 1992
ATTORNEY/AGENT INFORMATION:
NAME: COMSODAL, Kevin G.
REGISTRATION NUMBER: 34,033
REPRESENTATIVE NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628 5197
TELEFAX: 202 747 3528
TELEX: 248634
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: amino acid
STANDARDNESS: Single
COMPLEXITY: High
MULTIPLE TYPE: peptide
PCT US93-08528 30

Quality Match	24.1%	Score	410.5	DB	5	Length	326
Host Local Similarity	42.2%	Prod	No. 7.7e+28				
Matches	106	Conservative	6.5	Misses	1.87	Indels	21
						Gaps	9

[illegible]

Db	121	SLVIMVAIVAAAFVIAIMNDSTNVVSNKAGSCNITRC-FHREYEGSKAVLLIH-----IG	174
Q7	195	QVI-FWINEELVIVGYLLITKELYPSVFTGVRVPEPKVNRKVLIIAVTIGFPTIR	295
Db	175	IVLGEFVELLLEPTNI-VIIHTILGPKQGPNAEVFPALMVGVIVAVFVIGFVIRH	244
Q7	254	PARIVYIISQIRVDICIAENITLVYKKESTIIMLSIAACIDPTVYFPLKSTFSLISM	318
Db	234	IVOLEWITIAEL-GIMFESSNHCAINDARVYITGLSTIRVDEIVYVLLIKRIHNESEKT	272
Q7	314	KCFNEATSLSDNRRKEQDGGDFNEETFM	342
Db	293	NIMSSQKQSVYTRDTCTHMAIPIINHTIV	321

RESULT 15

US-08-088-R76-9
; Sequence 9, Application US/089888876
; Patent No. 6063596

```

1 GENERAL INFORMATION:
2 APPLICANT: Lal, Preeti
3 APPLICANT: Bandman, Oda
4 APPLICANT: Hillman, Jennifer L.
5 APPLICANT: Yue, Henry
6 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
7 TITLE OF INVENTION: WITH IMMUNE RESPONSE
8 NUMBER OF SEQUENCES: 9
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Incyte Pharmaceuticals, Inc.
11 STREET: 3174 Porter Drive
12 CITY: Palo Alto
13 STATE: CA
14 COUNTRY: USA
15 ZIP: 94304
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: diskette
18 COMPUTER: IBM Compatible
19 OPERATING SYSTEM: DOS
20 SOFTWARE: FASTSEQ for Windows Version 2.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/986,876
23 FILING DATE: Herewith
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE:
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Hillings, Lucy J.
30 REGISTRATION NUMBER: 36,749
31 REFERENCE/DOCKET NUMBER: PP-0441 US
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 650 855-0655
34 TELEFAX: 650-845-4166
35 TELFX:
36 INFORMATION FOR SEQ. ID NO: 9:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 342 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 IMMEDIATE SOURCE:
43 LIBRARY: GenBank
44 CLONE: 49443
45 US-08-986-876-9

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	Query Match	22.1%	Score 392.5;	Ht 3	Length 342;
	Post Local Similarity	30.7%	Pred. No 2;86		
Matches	10;	Conservative	66;	Mismatches	146;
				Indels	21;
Gaps					9

CY	20	DYKTVVAFPLATFLFVLGLITNLSAMRTIPQTL--PSS-SNEI-LETKNVISDLMILTT	76
		: : : : : :	
JB	10	DSEHYLVLPPIVSLIIPLVICLAVNCVIMWVARVPYSKRKLKEIKFFNNIVVALVTALVT	69
		:	



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OM protein - protein search, using sw model

Run on: August 21 2002, 15:38:37 Search time: 32.97 Seconds
(without alignments) 1152.176 Million cell updates/sec

Title: US-09-780-576-2
Percent score: 1778
Sequence: 1 MQAVENLTSPNTSLTRP.....SLDFPKKEDVDSHFNEETFM 342

Scoring table:
BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A.Geneseq_032802.*

1:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
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7:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSL/gcdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	20	AAW81576
2	1778	100.0	342	21	AAW71306
3	1778	100.0	342	21	AAH02840
4	1778	100.0	342	21	AAH94444
5	1778	100.0	342	22	AAW79239
6	1778	100.0	342	22	AAW94386
7	1748	98.3	342	21	AAV94445
8	1634	91.9	315	22	AAH04385
9	1528.5	86.0	343	22	AAH04384
10	1493.5	84.0	387	21	AAV94498
11	1237.5	69.6	267	22	AAE04387

ALIGNMENTS

RESULT	1	AAW81576	standard, Protein: 342 AA.
ID	AAW81576		
XX	AAW81576:		
XX	22-FEB-1999 (first entry)		
DE	EBV-Induced G-protein coupled receptor (EBI-2) polypeptide.		
XX	EBV-Induced G-protein coupled receptor, EBI-2; Epstein-Barr Virus; ulcer;		
KW	endothelium differentiation gene, FOS-1-like G protein coupled receptor;		
KW	recombinant; agonist; asthma, Parkinson's disease, heart failure; asthma;		
KW	hypotension; urinary retention; osteoporosis; antagonist; hypertension;		
KW	angina pectoris; myocardial infarction; allergy; psychosis; depression;		
KW	migraine; vomiting; stroke; eating disorder; migraine headache; cancer;		
KW	prostatic hypertrophy; detection; drug screening.		
XX			
OS	Homo sapiens.		
XX			
FX	Key	Location/Qualifiers	
FT	Misc-difference 6	/note- "encoded by ATT"	
FT	Misc-difference 14	/note- "encoded by AAC"	
XX			
PN	W09850549-A2.		
XX			
FX	12-NOV-1998.		
XX			
PE	07-MAY-1998; 9AWC-US09048.		
XX			
PP	07-MAY-1997; 97US-0852824.		
XX			


```

Db      1 mgavdhltsapnntslctrdykltqvlfpilylvlffvgtltnqlamrffqtrsknft 60
QY      61 IFKNTVTSULMLIFPEPKITSEAKLSTGPIPLEFWVWTSVIEFTMTYISISFLITTI 120
Db      61 IILKOLVSDLLMLITLPIKISDAKIQPIRLTTCQSLVLYLTMLYISISLIGLIT 120
QY      121 DRYQKTRTPPKTSNPKNI:GAKILSVVIAWPFULSLNMLITNRQPRDKVKKCSPIKS 180
Db      121 dryqktrtpktsnpknllgakiisvviwafmltlslpmlltnrpdckvkkcsfiks 180
QY      181 EELVMEHELVNYICQYIFMNFPIVVCVTLTKELRYSVVTPRVGKVKPRKKNVAVFI 240
Db      181 eglvwheivnyicqyifmfnfpivvcvtltkelysvvtprvgkvprkknvkvfi 240
QY      241 IIAVFICVPPHFAPIPYTLISQTRDVPDCTAENTLFWYKESTIMWTSLNACLDPPIYFF 300
Db      241 IIAVFICVPPHFAPIPYTLISQTRDVPDCTAENTLFWYKESTIMWTSLNACLDPPIYFI 300
QY      301 ICKSPRNSLSIMLKCPNSATSISQDNRRKKRQDGNPEETPM 342
Db      301 ICKSPRNSLSIMLKCPNSATSISQDNRRKKRQDGNPEETPM 342

RESULT 3
AA02840
ID      AA02840 standard; Protein; 342 AA.
XX
AC      AA02840;
XX
DT      22-AUG-2000 (first entry)
XX
DE      Human G protein-coupled receptor hGHR8 protein SEQ ID NO:34.
XX
KW      Human; G protein-coupled receptor; GPCR; transmembrane receptor;
KW      identification; agonist; screening; therapeutic; pharmaceutical;
KW      mutant.
XX
OS      Homo sapiens.
XX
PN      W0200022131 A2
PD      20-APR-2000.
XX
PE      13-OCT-1999; 99WO-US24065.
XX
PR      13-OCT-1999; qants-0170446.
PR      12-NOV-1999; qants-016029.
PR      20-NOV-1999; 98US-0109213.
PR      27-NOV-1999; 98US-0110060.
PR      16-FEB-1999; 99US-0120416.
PR      26-FEB-1999; qants-0121862.
PR      12-MAR-1999; 99US-0123944.
PR      12-MAR-1999; qants-0123945.
PR      12-MAR-1999; 99US-0123946.
PR      12-MAR-1999; 99US-0123949.
PR      12-MAR-1999; 99US-0123951.
PR      28-MAY-1999; qants-0136437.
PR      28-MAY-1999; 99US-0136439.
PR      28-MAY-1999; 99US-0137127.
PR      28-MAY-1999; qants-0137567.
PR      28-MAY-1999; qants-0141448.
PR      14-JUN-1999; 99US-0151114.
PR      27-AUG-1999; 99US-0152524.
PR      03-SEP-1999; 99US-0152524.
PR      29-SEP-1999; 99US-0156633.
PR      29-SEP-1999; 99US-0156655.
PR      29-SEP-1999; 99US-0156634.
XX
XX      (AREN-) ARENA PHARM INC.
PA
PI      Behan DB, Lehmman Huiusma K, Chalmers DJ, Chen K, Wang H;

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```

PI      Gore M, Liaw CW, Lin I, Howitz K, White C;
XX      WP1: 2990-317986/27.
DR      N-PSDB: AAA46034.
XX
PT      Non-endogenous, human G protein-coupled receptors for screening
PT      receptor, inverse or partial agonists useful as therapeutic agents
XX
PS      Example 1: Page 112-113; 187pp; English.
XX
CC      The present invention describes transmembrane receptors, preferably
CC      human G protein coupled receptors (GPCR), for which the endogenous
CC      ligand is unknown (orphan GPCR receptors). More specifically the present
CC      invention relates to non-endogenous, constitutively activated variants
CC      of a human GPCR. These non-endogenous human GPCRs can be useful for
CC      the direct identification of candidate compounds as receptor agonists,
CC      inverse agonists or partial agonists for use as pharmaceutical agents,
CC      AAA46017 to AAA46126 and AA02845 to AA02859 represent sequences used in
CC      the exemplification of the present invention.
XX
SQ      Sequence 342 AA:

Query Match      100.0%; Score 1778; DB 21; Length 342;
Best Local Similarity 100.0%; Ident. No. 4; 2e-187;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MQAVDNLTSAPGNTSLCTRDYKITQVLEPLLTYLFEFGILTNGLAMRIFQIRSKNFI 60
Db      1 mgavdhltsapnntslctrdykltqvlfpilylvlffvgtltnqlamrffqtrsknft 60
QY      61 IFKNTVTSULMLIFPEPKITSEAKLSTGPIPLEFWVWTSVIEFTMTYISISFLITTI 120
Db      61 IILKOLVSDLLMLITLPIKISDAKIQPIRLTTCQSLVLYLTMLYISISLIGLIT 120
QY      121 DRYQKTRTPPKTSNPKNI:GAKILSVVIAWPFULSLNMLITNRQPRDKVKKCSPIKS 180
Db      121 dryqktrtpktsnpknllgakiisvviwafmltlslpmlltnrpdckvkkcsfiks 180
QY      181 EELVMEHELVNYICQYIFMNFPIVVCVTLTKELRYSVVTPRVGKVKPRKKNVAVFI 240
Db      181 eglvwheivnyicqyifmfnfpivvcvtltkelysvvtprvgkvprkknvkvfi 240
QY      241 IIAVFICVPPHFAPIPYTLISQTRDVPDCTAENTLFWYKESTIMWTSLNACLDPPIYFF 300
Db      241 IIAVFICVPPHFAPIPYTLISQTRDVPDCTAENTLFWYKESTIMWTSLNACLDPPIYFI 300
QY      301 ICKSPRNSLSIMLKCPNSATSISQDNRRKKRQDGNPEETPM 342
Db      301 ICKSPRNSLSIMLKCPNSATSISQDNRRKKRQDGNPEETPM 342

RESULT 4
AA02840
ID      AA02840 standard; Protein; 342 AA.
XX
AC      AA02840;
XX
DT      21-AUG-2000 (first entry)
XX
DE      Human 15625 receptor protein.
XX
KW      Human; G protein-coupled receptor; GPCR; 15625 receptor protein;
KW      glial cells; spleen; colon; liver; brain; T-cell; heart;
KW      red cell; thymus; B-cell; pancreas; disordered; chromosome 3;
KW      dracmia, neutropenia; thrombocytopenia, gene therapy; ss.
XX
OS      Homo sapiens.
XX
XX      Key Location/Qualifiers
XX      FH 1..25
XX      FT Domain
XX      FT Modified-site 6..9

```

FT /label= N-glycosylation
 FT Misc difference 14
 FT /label= "Encoded by AGC"
 FT 13..16
 FT Modified site
 FT /label= N-glycosylation
 FT 26..402
 FT Domain
 FT /label= Transmembrane-domain
 FT 49..44
 FT Modified site
 FT /label= N-myristoylation
 FT 121..123
 FT Modified site
 FT /label= C-myc signal transduction site
 FT 126..128
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 161..165
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 174..176
 FT Modified site
 FT /label= protein_kinase_phosphorylation
 FT 404..442
 FT Domain
 FT /label= Intracellular-domain
 FT 404..406
 FT Modified site
 FT /label= protein_kinase_C_phosphorylation
 FT 341..348
 FT /label= N-myristoylation

W0200028028 A1

18 MAY 2000.

05 NOV 1999: 99W0-0825956.

06 NOV 1999: 98US 0187134.

25 AUG 1999: 99US 0182918.

(MILL.) MILLENNIUM PHARM INC.

Glucksmann MA, Gu W, Welch NS;

WPI: 2000 476543/42.

N-PSDB: AAA27126.

Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia -

Disclosures: Page 88 89; 97pp; English.

The present sequence shows the 15625 receptor protein. It is a novel G coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynucleotides and polypeptides include anaemia, neutropenia and thrombocytopenia.

XX Sequence 442 AA;

Query Match 100.0%; Score 1778; DH 21; Length 342;

Best Local Similarity 100.0%; Prev. No. 4,2e-187;

Motives 442; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 MOAVALNTSACNTSLTTRPKITGVVFLPLVTLFVGLITKILAMRIFQIRSKNFI 60

10b 1 mgvavntlsapntslstrgkltgvtlpllygtvltfvtltnqlamrtitfgtrsksnfi 60

UY 61 IETKNTVLSQMLITFPRKILISPAKLGTPLEFVGVYTVSVIFETMTYISIFGLTIT 120

Db 61 IILKULVSLDMLIIIPKILSDAKLQTPRLIVCGVSLVLYLUMYISILQLII 120
 QY 121 DRYOKTRPRPKTSNPKNILGAKILSVIWAHPFLLSLNMLITNRPDKVKKCSPLKS 180
 Db 121 dlygktrprpktsnpknilyakilsvlwafnrlslpmlltnqpdvknvksstlks 180
 QY 181 EFGLVWHEIVNTYCOVTFWNIPLIVIVCYTLITKELYSYVTRGVKVPKKYVWYFI 240
 Db 181 efglvwheivnyicqvtfwntfplivivcytlitkelysyvtrgvkvppkknvxfi 240
 QY 241 ITAVPFICVPPHAPARIPITLSQTRDVPCTAENLIFVKKSTIMVSIACIDPITPF 300
 Db 241 IIAVITICVPHIARIPYLSQTRDVIDCAENLIIYKESLIWLSINACIDPILYLI 300
 QY 301 ICKSPKNSLISMICKNSATSLSDPNKKKKFQDGGDPNEETPM 342
 Db 301 Icksfnsllsmickpnsatsslsqdrkkqygdppneetpm 342

RESULT 5

AAW79249

ID AAW79249 standard; Protein; 342 AA.

AAW79249;

06-NOV-2001 (first entry)

Human protein SEQ ID NO 1911.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;

vacine; peptide therapy; stem cell growth factor; haematopoiesis;

tissue growth factor; immunomodulatory; cancer; leukemia;

nervous system disorder; arthritis; inflammation.

Homo sapiens.

W0200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US04098.

03-FEB-2000; 2000US-0446414

27-APR-2000; 2000US-0560875

20-JUN-2000; 2000US-0596075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0664561.

20-OCT-2000; 2000US-0694325

30-NOV-2000; 2000US-0728422.

(HSE-) HYSEQ INC.

Tang YT, Liu C, Dermanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;

Zhao QJ, Wang D, Mao J, Zhang J, Ren F, Chen R, Wang ZW;

Xue AJ, Yang Y, Wejhuman T, Goodrich R;

WPI: 2001 476283/51.

N-PSDB: AAK52182.

Nucleic acids encoding polypeptides with cytokine-like activities,

useful in diagnosis and gene therapy -

Claim 20; Page 4310, 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK54435) and the encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and

CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizophrenia, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is a fragment of human
 CC P2-purine-gc receptor subtype, referred as P2Y12.
 XX
 XX Sequence 315 AA;

Query Match 91.9% Score 1634 DB 22 Length 315;
 Best Local Similarity 100.0%; Pred No. 2, 6e-171;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MGAVNLTSAPDNTSICITRDYKIQVLEPLLYTVLPFGVLTNGIAMIPOIRKSNFI 60
 |||||||
 DB 1 mgavnltsapnslctrdyklqvlpllyvltngiamlilqlrksnfi 60
 |||||||
 DB 61 IFLKNTVISDLMLITFPEKIIISDAKICGPIKPFVCOVTSVIFPYMVISISPLGII 120
 |||||||
 DB 61 flkntvisdlmlitfpkiiisdakicgpiirfvqvtsvifpymsisplgiti 120
 |||||||
 DB 121 DRYQVITTRPKSNKNLGAKITSVIMAFMELSLNMTLNQPDKNVKKSELS 180
 |||||||
 DB 121 dryqvitrpkksnknlgakitsvimaflmslntnqpdknvkksefiks 180
 |||||||
 DB 181 EFGIWMHEIVNYICQVIMNFIIVCYTLITKELYSYVRGCVGVPKKVWVKEI 240
 |||||||
 DB 181 efgiwmheivnyicqvimnfiivcytlitkelysyrvgcvgvpkkvwvkei 240
 |||||||
 DB 241 IIAVFICVPHFPHARIPYTLISQINDVPCIAENILFYVKSTLMLTISIACLDPIYVF 300
 |||||||
 DB 241 iiavficvphfpharipytlisqindvpciaenilfyvkstlmltisiacldpiyvf 300
 |||||||
 DB 301 LKSEFNSLSMLKC 315
 |||||||
 DB 301 lksefnslsmlkc 315

RESULT 9
 AAE04384
 ID AAE04384 standard; protein: 343 AA.

AC AAE04384;
 XX
 XX 04-SEP-2001 (first entry)
 DT
 XX
 XX Rat P2 purine-gc receptor subtype, P2Y12.

XX Rat; P2-purine-gc receptor, P2Y12, candidate; vasodilator; thrombolytic;
 XX cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
 XX myocardial infarction; ischemic attack; pre-eclampsia; bleeding disorder;
 XX carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 XX vascular injury; schizophrenia; eating disorder; depression; anisotlasia;
 XX peripheral vascular disease; platelet aggregation; restenosis; embolism;
 XX thrombocytopenic purpura; stroke; post-thrombotic toxin sensitive G protein;
 XX G1; disseminated intravascular coagulation; thrombosis.

XX
 XX Patisu notvegious
 XX
 XX WO200146454-A1.

XX
 XX 28-JUN-2001.

XX
 XX 26-DEC-2000; 2000WO-US34998.

XX
 XX 23-DEC-1999; 99US-0171622.

XX
 XX (COPY-) COR THRAPPEUTICS INC.

XX
 XX Conley PB, Janzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Holloper G;
 XX
 XX WPL, 2001-418082/44.
 UK N-PSUB; AAD08b93.
 XX
 XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
 PT for identifying binding partners and for diagnostic applications
 XX
 XX Claim 14; Page 81-82; 108pp; English.

CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purine-gc receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin-
 CC sensitive G protein (Gi). P2Y12 receptor is a G protein coupled receptor
 CC that responds to ADP. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischaemic
 CC attacks, strokes, peripheral vascular disease, pre-eclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 CC thrombocytopenic purpura or a bleeding disorder, thrombotic and
 CC restenotic complications following angioplasty, carotid endarterectomy,
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
 CC stent placements or insertion of endovascular devices and prostheses.
 CC P2Y12 receptor is useful for identifying binding partners and for
 CC diagnostic applications. P2Y12 receptor provides targets for screening
 CC synthetic small molecules and combinatorial or naturally occurring
 CC compound libraries to regulate platelet aggregation, vascular injury, or
 CC disease as well as schizophrenia, eating disorders, depression, migraine
 CC and other brain disorders. The present sequence is rat P2-purine-gc
 CC receptor subtype, referred as P2Y12 receptor.
 XX
 XX Sequence 343 AA;

Query Match 86.0%; Score 1528.5; DB 22 Length 343;
 Best Local Similarity 86.9%; Pred. No. 1, 2e-159;
 Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

DB 6 NITSAPDNTSICITRDYKIQVLEPLLYTVLPFGVLTNGIAMIPOIRKSNFI 65
 |||||||
 DB 12 ntsipgntslcsrdyklqvlpllyvltngiamlilqlrksnfi 65
 |||||||
 DB 66 TVISDLMLITFPEKIIISDAKICGPIKPFVCOVTSVIFPYMVISISPLGII 125
 |||||||
 DB 72 tvisdmlitfpkiiisdakicgpiirfvqvtsvifpymsisplgiti 125
 |||||||
 DB 126 TIRPKTSNPKNLGAKITSVIMAFMELSLNMTLNQPDKNVKKSELS 185
 |||||||
 DB 132 tlrfpktsnknlgakitsvimaflmslntnqpdknvkksefiks 185
 |||||||
 DB 186 WHIIVNYICQVIMNFIIVCYTLITKELYSYVRGCVGVPKKVWVKEI 245
 |||||||
 DB 192 whiivnyicqvimnfiivcytlitkelysyrvgcvgvpkkvwvkei 245
 |||||||
 DB 246 FICVPHFPHARIPYTLISQINDVPCIAENILFYVKSTLMLTISIACLDPIYVF 305
 |||||||
 DB 252 ficvphfpharipytlisqindvpciaenilfyvkstlmltisiacldpiyvf 305
 |||||||
 DB 306 RNSLSMLKCPNSATSLSDNRKKEDGSDPNETPM 342
 |||||||
 DB 312 rnslsmlkcpnsatslsdnrkkedgdpnetpm 343

RESULT 10

AAV94498
 ID AAV94498 standard; protein: 387 AA.

XX
 XX AAV94498;

XX
 XX 15-SEP-2000 (first entry)

XX
 XX Rat MP-10 receptor protein.

QY 1 MGVAVNLISAGNTSLCTROKKITOVLEPLLYTVLFPVGLITNGLAMPFPQIPKSNFI 60
 DB 1 mgavnlhsagntslctrdykitqvlfpllyvltfvglitnglamrffqirsksnfi 60
 QY 61 IFLKNTVISDLMLITPEFKILSDAKLTGRLRTFVCQVTSVFIFPMWISISFLGIIIT 120
 DB 61 iflknvtsdlmlitpelfkilsdakltgtrlrfvcqvtsvlfpmwisistflgiiit 120
 QY 121 DRYOKTTRPRTSNKNLIGAKLISVIMAFMPLISLPMNITINROPRDNKVKCSFLKS 180
 DB 121 dryokttrprikspnknligaklsvswafmplislpnmilitnropdrdnkvkcsflks 180
 QY 181 EFGLEWHEIVNYICQVIFMINELIVTVYTLITRELYRSVPTPVGKVKPKKYNKVF 240
 DB 181 efglewheivnyicqvifminelivtvvtlitrlyrsvptpvgkvkpkkynkvf 240
 QY 241 IIAVTTI-CFVFF 252
 DB 241 hecllyltsipd 253

RESULT 12

ID AAB23029 standard; Protein: 333 AA

AC AAB23029;

DT 16-JAN-2001 (first entry)

DE Human chemokine receptor-like protein, SECX 2777610.

XX SECX protein; human; secreted; membrane-associated; cancer;
 XX proliferation regulator; differentiation regulator; non-malignant tumour;
 XX immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 XX infection; inflammatory disorder; arthritis; haematopoietic disorder;
 XX skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 XX neurological disease; Alzheimer's disease; trauma; wounding;
 XX spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 XX anti-HIV; anti-inflammatory; antirheumatic; antileukosclerotic;
 XX neuroprotective; vintory; antiallergic; antimicrobial; cardiac;
 XX dermatological; gene therapy.

XX Homo sapiens.

XX W0200053742-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000W-11S05280.

XX 09-MAR-1999; 9905-0123667.

XX 08-MAR-2000; 2000US-0123667.

XX (CURA-) CURAGEN CORP.

XX Shimkels RA;

XX WPI: 2000-594318/56.

XX N-PSDB: AAA93616.

XX Novel human membrane associated or secreted polypeptides and

XX polynucleotides useful for diagnosis, prevention and treatment of

XX neurological disorders such as cancer, immune, cardiovascular and

XX Claim 1: Fig 1: 151pp; English.

XX Sequences AAB23029-823048 represent human SECX proteins. The SECX
 CC proteins of the invention are either secreted or membrane-associated
 CC and act as regulator of cellular proliferation and
 CC differentiation. SECX proteins or nucleotides are useful for diagnosing
 CC the presence of, or predisposition to, a disease associated with altered

CC levels of SECX proteins and nucleotides. The SECX proteins are also
 CC useful to screen compounds that modulate SECX activity or expression. The
 CC interaction of a SECX protein with other cellular proteins may be useful
 CC to modulate the activity of a partner protein. SECX nucleotides are useful
 CC for the recombinant expression of SECX protein, and may be used to detect
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
 CC nucleic acid sequences are also useful for identifying a cell or tissue
 CC type in a biological sample, and in forensic biology. SECX primers or
 CC probes are useful for detecting the presence of SECX nucleotides and for
 CC screening tissue cultures for contamination. Diseases that may be treated
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.

CC Sequence 333 AA;

CC Query Match 46.6%, Score 829; DB 21; Length 333;

CC Best Local Similarity 49.1%, Fred. No. 1.1e-82;

CC Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CTRDYKITOVLEPLLYTVLFPVGLITNGLAMPFPQIPKSNFI1ELKNVTSIDLMLIT 76

DB 15 mgavnlhsagntslctrdykitqvlfpllyvltfvglitnglamrffqirsksnfi 74

QY 77 FPKKILSDAKLTGRLRTFVCQVTSVFIFPMWISISFLGIIITDRYOKTTRPRTSNKN 136

DB 75 iflknvtsdlmlitpelfkilsdakltgtrlrfvcqvtsvlfpmwisistflgiiit 134

QY 137 EFGLEWHEIVNYICQVIFMINELIVTVYTLITRELYRSVPTPVGKVKPKKYNKVF 196

DB 135 efglewheivnyicqvifminelivtvvtlitrlyrsvptpvgkvkpkkynkvf 194

QY 197 IPWNLPLIVVYCYTLITKELYSRVYRTRGVKVKKYNKVF11AVPTCPVPHRFA 256

DB 195 ifwvnlplivvyvyltkelyrsrvytrgvkvkknvkvf11avptcpvphrf 254

QY 257 IPYTLISOTRDPVPOCTANPLFYVKSPLMTSLNACIDPFIYFPLCKSPRNSI1SMLKCP 316

DB 255 vpytlisotrdvpvpoctanplfyvksplmtslnacidpfiyfplcksprnsi 312

QY 317 NSATSLSDQNRKKEOD 332

DB 313 nkatlsdqnrkkesqd 328

RESULT 13

ID AAB74397 standard; Protein: 333 AA.

AC AAB74397;

DT 11-JUL-2001 (first entry)

DE Human G protein coupling receptor.

XX Human; G protein coupling receptor; CNS; central nervous system.

XX Homo sapiens.

XX JP2001054389-A.

XX 27-FEB-2001.

XX 17-AUG-1999; 99JF-0230777.

17 AUG 1999: 99JP 0280777.
 XX
 PA (YAMA) YAMAMOTOCHI PHARM CO LTD.
 XX
 DR WPI: 2001-21019/44
 DR N-PSDB: AAB87601.
 XX
 PT A novel G protein coupled receptor.
 XX
 PS Claim 1: Page 11: Japp: Japanese.
 XX
 CC The present invention relates to a novel G protein coupled
 CC receptor, a gene encoding for the receptor family, a process for
 CC preparation of the receptor family, an antibody to the receptor
 CC family and a method for screening using the receptor. The invention may
 CC be used for screening of agents expected to be useful for
 CC prevention and treatment of central nervous system (CNS) diseases.
 CC The present sequence the G protein coupled receptor.
 XX
 Sequence: 333 AA.

Query Match 46.6%; Score 829; DB 22; Length 333;
 Best local Similarity 49.1%; Pred. NO. 1: 82;
 Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

17 CTGKVKITGVLEPLLYTLFFVGLITNGLAMRLEFQIRSKSNPIFLKNTVISDLMLLT 76
 15 CPDRIIVGVLPALYVGVLTGIIINLALWLVHPSSSTIIYIKNLVADIMLM 74
 77 FPFKILSDAKLGTPRTFVCQVTISVIFPTMYISISFLGITIDRQKTRPKTSNPK 136
 75 Ipfkllssshlpwlpwltatvcrissvilyetmyqvalqladrlklirpmlilk 134
 137 NLGAKKILSVVIMAWMELISIPNMLITNRPDKNVKCKSLKSEFGLWHEIVNYICQV 196
 135 kpvltakvslilwllllisipmlisnkeatpsvkkcaalkpqlakwhqmnatcql 194
 197 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 256
 195 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 254
 257 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 316
 255 VPTLSTQTRVDCTAENTLYFVKESTIMLTSLNACIDPFIYFLCKSFNSLSMLKCP 316
 317 NSATSLSDNNKKKQD 332
 313 RKTASSGQNSGQD 328

RESULT 14
 ID AAB/4494 standard; Protein: 333 AA.
 AC AAB/4494;
 XX
 DE 11 MAY 2001 (first entry)

XX Novel human G protein coupled receptor.
 XX Human G protein coupled receptor; central nervous system disease;
 XX schizophrenia; Parkinson's disease.
 XX Homo sapiens.
 XX ID: 2001029083 A.
 XX
 XX 06 FEB 2001.
 XX
 XX 24 JUL 1999: 99JP 0209918.
 XX
 XX 24 JUL 1999: 99JP 0209918.

XX
 PA (YAMA) YAMAMOTOCHI PHARM CO LTD.
 XX
 DR WPI: 2001-221494/23.
 DR N-PSDB: AAB81501.
 XX
 PT A new G protein coupled receptor.
 XX
 PS Example 1: Page 11: Japp: Japanese.
 XX
 CC The present invention provides the protein and coding sequences for a
 CC novel human G protein coupled receptor. This is useful in the
 CC identification of treatments for central nervous system diseases such as
 CC schizophrenia, Parkinson's disease and achos.
 XX
 Sequence: 333 AA;

Query Match 46.6%; Score 829; DB 22; Length 333;
 Best local Similarity 49.1%; Pred. NO. 1: 82;
 Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

17 CTGKVKITGVLEPLLYTLFFVGLITNGLAMRLEFQIRSKSNPIFLKNTVISDLMLLT 76
 15 CPDRIIVGVLPALYVGVLTGIIINLALWLVHPSSSTIIYIKNLVADIMLM 74
 77 FPFKILSDAKLGTPRTFVCQVTISVIFPTMYISISFLGITIDRQKTRPKTSNPK 136
 75 Ipfkllssshlpwlpwltatvcrissvilyetmyqvalqladrlklirpmlilk 134
 137 NLGAKKILSVVIMAWMELISIPNMLITNRPDKNVKCKSLKSEFGLWHEIVNYICQV 196
 135 kpvltakvslilwllllisipmlisnkeatpsvkkcaalkpqlakwhqmnatcql 194
 197 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 256
 195 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 254
 257 IFTWIFLIVGYTITFELRSYVPTGKVGKPKKVVKVFITIAVFETVFEHAR 316
 255 VPTLSTQTRVDCTAENTLYFVKESTIMLTSLNACIDPFIYFLCKSFNSLSMLKCP 316
 317 NSATSLSDNNKKKQD 332
 313 RKTASSGQNSGQD 328

RESULT 15
 ID AAE02494 standard; Protein: 333 AA.
 AC AAE02494;
 XX
 DE 10-AUG-2001 (first entry)

XX Human G protein coupled receptor; GPCR; GPCR; GPCR; GPCR; GPCR;
 XX neuroleptic; neuroleptic; neuroleptic; bipolar disease; psychotropic;
 XX neurological disorder; psychiatric disorder; neurosis; anxiety; neuritis;
 XX attention deficit hyperactivity disorder; neurosis; neurosis; neurosis;
 XX affective disorder; neuroleptic; Alzheimer's disease; Parkinson's disease;
 XX depression; migraine; genetic screening; chromosome 3.
 XX Homo sapiens.
 XX
 XX Key location/Qualifiers
 XX 29..53
 XX /label- Transmembrane-domain_(1TM)
 XX 54..62
 XX /label- Intracellular-domain
 XX /note- "first IC loop"
 XX 63..82
 XX Domain

FT /label= Transmembrane_domain_(21M)
 FT 83..96
 FT /label= Extracellular_domain
 FT /note= "First EC loop"
 FT 97..118
 FT /label= Transmembrane_domain_(31M)
 FT 119..135
 FT /label= Intracellular_domain
 FT /note= "Second IC loop"
 FT 136..160
 FT /label= Transmembrane_domain_(41M)
 FT 161..188
 FT /label= Extracellular_domain
 FT /note= "Second EC loop"
 FT 189..211
 FT /label= Transmembrane_domain_(51M)
 FT 212..231
 FT /label= Intracellular_domain
 FT /note= "Third IC loop"
 FT 232..252
 FT /label= Transmembrane_domain_(61M)
 FT 253..286
 FT /label= Extracellular_domain
 FT /note= "Third EC loop"
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 FT 14921..14940
 FT 14941..14960
 FT 14961..14980
 FT 14981..15000
 FT 15001..15020
 FT 15021..15040
 FT 15041..15060
 FT 15061..15080
 FT 15081..15100
 FT 15101..15120
 FT 15121..15140
 FT 15141..15160
 FT 15161..15180
 FT 15181..15200
 FT 15201..15220
 FT 15221..15240
 FT 15241..15260
 FT 15261..15280
 FT 15281..15300
 FT 15301..15320
 FT 15321..15340
 FT 15341..15360
 FT 15361..15380
 FT 15381..15400
 FT 15401..15420
 FT 15421..15440
 FT 15441..15460
 FT 15461..15480
 FT 15481

